UNITED STATES PROVISIONAL PATENT APPLICATION

for

METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE CALCINEURIN INTERACTING PROTEIN (MCIP)

by

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BACKGROUND OF THE INVENTION

1. Field of the Invention

The present invention relates generally to the fields of developmental biology and molecular biology. More particularly, it concerns the proteins, classified here as MCIPs, identified as regulating calcineurin function.

2. Description of Related Art

Calcineurin is a serine/threonine protein phosphatase that plays a pivotal role in developmental and homeostatic regulation of a wide variety of cell types (Klee *et al.*, 1998; Crabteee, 1999). The interaction of calcineurin with transcription factors of the NFAT family following activation of the T cell receptor in leukocytes provides the best characterized example of how calcineurin regulates gene expression (Rao *et al.*, 1997). Changes in intracellular calcium promote binding of Ca^{2+}/calmodulin to the catalytic subunit of calcineurin (CnA), thereby displacing an autoinhibitory region and allowing access of protein substrates to the catalytic domain. Dephosphorylation of NFAT by activated calcineurin promotes its translocation from the cytoplasm to the nucleus, where NFAT binds DNA cooperatively with an AP1 heterodimer to activate transcription of genes encoding cytokines such as IL-2. This basic model of NFAT activation has been shown to transduce Ca2+ signals via calcineurin in many cell types and to control transcription of diverse sets of target genes unique to each cellular environment (Timmerman *et al.*, 1996). In each case, NFAT acts cooperatively with other transcription factors that include proteins of the AP1 (Rao *et al.*, 1997), cMAF (Ho *et al.*, 1996), GATA (Mesaeli *et al.*, 1999; Molkentin *et al.*, 1998; Musaro *et al.*, 1999), or MEF2 (Chin *et al.*, 1998; Liu *et al.*, 1997; Mao *et al.*, 1999; Mao and Wiedmann, 1999) families. In addition to T cell activation, cellular responses controlled by calcineurin signaling include synaptic plasticity (Mao *et al.*, 1999; Graef *et al.*, 1999; Zhuo *et al.*, 1999) and apoptosis (Wang *et al.*, 1999; Youn *et al.*, 1999).

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Recent studies of calcineurin signaling in striated myocytes of heart and skeletal muscle have expanded the scope of important physiological and pathological events controlled by this ubiquitously expressed protein. Forced expression of a constitutively active form of calcineurin in hearts of transgenic mice promotes cardiac hypertrophy that progresses to dilated cardiomyopathy, heart failure, and death, in a manner that recapitulates features of human disease (Molkentin et al., 1998). Moreover, hypertrophy and heart failure in these animals, and in certain other animal models of cardiomyopathy, are prevented by administration of the calcineurin antagonist drugs cyclosporin A or FK-506 (Sussman et al., 1998). In skeletal muscles, calcineurin signaling is implicated both in hypertrophic growth stimulated by insulin-like growth factor-1 (Musaro et al., 1999; Semsarian et al., 1999), and in the control of specialized programs of gene expression that establish distinctive myofiber subtypes (Chin et al., 1998; Dunn et al., 1999). These observations have stimulated interest in the therapeutic potential of modifying calcineurin activity selectively in muscle cells while avoiding unwanted consequences of altered calcineurin signaling in other cell types (Sigal et al., 1991).
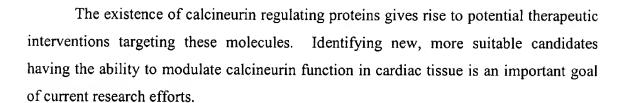
The activity of calcineurin in mammalian cells can be modulated by interactions with other proteins. These include not only immunophilins that are the targets of the immunosuppresant drugs cyclosporin A and FK-506, but two unrelated proteins (AKAP79 and cabin-1/cain) that were identified recently. AKAP79 binds calcineurin in conjunction with protein kinase C and protein kinase A, serving as a scaffold for assembly of a large hetero-oligomeric signaling complex (Kashishian et al., 1998). Cabin-1/cain binds both calcineurin and the transcription factor MEF2 (Sun et al., 1998; Lai et al., 1998). As a consequence of cabin-1 overexpression, calcineurin activity is inhibited and MEF2 is sequestered in an inactive state. Another calcineurin-binding protein is Rex1p (YKL159c) of Saccharomyces cerevisiae. A preliminary report noted that this small 24 kDa protein inhibits calcineurin signaling when overexpressed in yeast (Kingsbury and Cunningham, 1998).

The existence of calcineurin regulating proteins gives rise to potential therapeutic interventions targeting these molecules. Identifying new, more suitable candidates having the ability to modulate calcineurin function in cardiac tissue is an important goal of current research efforts.

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SUMMARY OF THE INVENTION

Therefore, according to the present invention, there is provided a method of screening for a modulator of MCIP binding to calcineurin comprising (a) providing an
10 MCIP and calcineurin; (b) admixing the MCIP and calcineurin in the presence of a candidate modulator; (c) measuring MCIP/calcineurin binding; and (d) comparing the binding in step (c) with the binding of MCIP and calcineurin in the absence of said candidate modulator, whereby a difference in the binding of MCIP and calcineurin in the presence of said candidate modulator, as compared to binding in the absence of said
15 candidate modulator, identifies said candidate modulator as a modulator of MCIP binding to calcineurin. In one embodiment, the MCIP and calcineurin are part of a cell free system. In another embodiment, the MCIP and calcineurin are located within an intact cell, for example, in a animal. Useful cells include myocytes, cardiomyocytes, H9C2 cells, neonatal cardiomyocytes, 3T3 cells, 293 cells and myotube cells.

20   The modulator may increase or decrease MCIP binding to calcineurin. Either or both MCIP and calcineurin may be labeled, for example, one with a quenchable label and . the other with a quenching agent. Alternatively, where both MCIP and calcineurin are labeled, the labels are not detectable unless brought into proximity of each other. The cell may be engineered to overexpress MCIP, calcineurin or both. The method may
25 comprises immunologic detection of MCIP, calcineurin or both. The MCIP may be MCIP1, MCIP2 or MCIP3.

In another aspect of the invention, there is provided a method of screening for a modulator of MCIP dephosphorylation comprising (a) providing a phosphorylated MCIP and calcineurin; (b) admixing the MCIP and calcineurin in the presence of a candidate
30 modulator; (c) assessing MCIP phosphorylation; and (d) comparing the phosphorylation

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state of MCIP in step (c) with the phosphorylation state of MCIP in the absence of the candidate modulator, whereby a difference in MCIP phosphorylation in the presence of said candidate modulator, as compared to phosphorylation in the absence of said candidate modulator, identifies said candidate modulator as a modulator of MCIP phosphorylation.

The modulator may increase or decrease MCIP dephosphorylation by calcineurin. The intact cell may express a protein selected from the group consisting of PKC, CaMK, GSK3 and MAPK, and isoforms and variants thereof. The intact cell also may be engineered to overexpress one or more of MCIP and calcineurin. The assessing may comprise detection of radiolabeled phosphorus, detection of changes of electrophoretic mobility, or detection of binding by antibodies that discriminate between phosphorylation states. The MCIP may be MCIP1, *e.g.*, with phosphorylation at Ser108 assessed, MCIP2 or MCIP3.

In yet another aspect of the invention, there is provided a method of screening for a modulator of MCIP expression comprising (a) providing a cell expressing an MCIP and calcineurin; (b) administering to said cell a candidate modulator; (c) measuring MCIP expression; and (d) comparing the expression in step (c) with the expression of MCIP in the absence of the candidate modulator, whereby a difference in MCIP expression in the presence of said candidate modulator, as compared to expression in the absence of said candidate modulator, identifies said candidate modulator as a modulator of MCIP expression.

The cell may be a myocyte or a cardiomyocyte. The measuring of MCIP expression may comprise assessing transcription by Northern analysis, assessing transcription by quantitative RT-PCR, ELISA, or Western blot. The MCIP may be selected from the group consisting of MCIP1, MCIP2 and MCIP3. The modulator may increase or decrease MCIP expression.

In still yet another aspect of the invention, there is provided a method of screening for a modulator of muscle cell growth comprising (a) providing a cell expressing an MCIP and calcineurin; (b) administering to said cell a candidate modulator; (c)

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measuring transcription of a target molecule that is indicative of muscle cell growth; and

(d) comparing the transcription in step (c) with the transcription of the target molecule in the absence of the candidate modulator, whereby a difference in muscle cell growth in the presence of said candidate modulator, as compared to growth in the absence of said

5   candidate modulator, identifies said candidate modulator as a modulator of muscle cell growth.

The cell may be a myocyte or a cardiomyocyte. The method may further comprise measuring transcription of the target molecule in the absence of the candidate inhibitor, for example, MEF2. The MCIP may be MCIP1, MCIP2 or MCIP3. The

10   modulator may increase or decrease muscle cell growth. The cell may be located in a mammal.

In each of the preceding screening embodiments, there also is provided similar methods for the production of a modulator, comprising each of the aforementioned screening steps, followed by the additional step of producing the modulator so identified.

15   In another aspect of the invention, there is provided a method of modulating muscle cell growth comprising (a) providing a modulator of MCIP binding to calcineurin; and (b) administering said modulator to a muscle cell, whereby administration of said modulator results in modulation of muscle cell growth.

In another aspect of the invention, there is provided a method of modulating

20   muscle cell growth comprising (a) providing a modulator of MCIP dephosphorylation by calcineurin; and (b) administering said modulator to a muscle cell, whereby administration of said modulator results in modulation of muscle cell growth.

In another aspect of the invention, there is provided a method of modulating

25   muscle cell growth comprising (a) providing a modulator of MCIP expression; and (b) administering said modulator to a muscle cell, whereby administration of said modulator results in modulation of muscle cell growth.

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The muscle cell may be located in a mammal. The modulator may be an agonist of muscle cell growth, for example, a small molecule, or an expression cassette comprising a DNA segment encoding an MCIP operably linked to a promoter active in said muscle cell. The promoter may be myosin light chain-2 promoter, alpha actin promoter, troponin 1 promoter, Na^+/Ca^{2+} exchanger promoter, dystrophin promoter, creatine kinase promoter, alpha7 integrin promoter, brain natriuretic peptide promoter, alpha B-crystallin/small heat shock protein promoter, atrial natriuretic factor promoter or alpha myosin heavy chain. The expression cassette may further comprise a polyadenylation signal or an origin of replication. The expression construct may be a viral expression construct; for example, an adenoviral construct, a retroviral construct, an adeno-associated viral construct, a herpesviral construct, a vaccinia viral construct, a polyoma viral construct, or a Sindbis viral vector. The method further comprises administering to said mammal a pharmaceutical agent used to treat cardiac disease.

In a further aspect of the invention, there is provided an isolated and purified DNA segment encoding a MCIP1 promoter, such as that isolatable from the sequence of SEQ ID NO:11. Also provided is an expression cassette comprising 50-1000 base pairs of SEQ ID NO:11 operably linked to a DNA segment encoding a polypeptide other than MCIP1. The polypeptide may be screenable marker protein. A host cell comprising an expression cassette comprising 50-1000 base pairs of SEQ ID NO:11 operably linked to a DNA segment encoding a polypeptide other than MCIP1 also is provided.

In yet a further aspect of the invention, there is provided a method for screening for modulators of MCIP1 expression comprising (a) providing a cell transformed with an expression cassette comprising 50-1000 base pairs of SEQ ID NO:11 operably linked to a DNA segment encoding a screenable marker protein; (b) administering to said cell a candidate modulator; (c) measuring expression of said marker protein; and (d) comparing the expression of said marker protein in step (c) with the expression of said marker protein in the absence of said candidate modulator, whereby a difference in marker protein expression in the presence of said candidate modulator, as compared to expression in the absence of said candidate modulator, identifies said candidate modulator as a modulator of MCIP expression.

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In still yet a further asepct of the invention, there is provided a method of treating cardiac hypertrophy or heart failure comprising administering to a subject suffering from cardiac hypertrophy or heart failure an agent that promotes MCIP binding to calcineurin. The method may further comprise treating said subject with an ionotrope, a beta blocker,

5   an antiarrhythmic, a diuretic, a vasodilator, a hormone antagonist, an endothelin antagonist, an angiotensin type 2 antagonist or a cytokine inhibitor/blocker. The agent may be a phosphatase that acts on Ser108 of MCIP, an inducer of a phosphatase that acts on Ser108 of MCIP, a MCIP analogue that binds calcineurin but lacks a removable phosphate at Ser108, or an expression cassette comprising an MCIP coding sequence

10   under the control of a promoter active in cardiac tissue. The agent may be administered intravenously or orally, may be in a delayed release formulation. The agent may be a small molecule modulator.

In another aspect of the invention, there is provided an isolated and purified nucleic acid encoding an MCIP1 polypeptide that lacks sequences encoded by Exons 1, 2

15   and 3. The nucleic acid may further comprise a promoter, for example, a muscle specific promoter, for example, myosin light chain-2 promoter, alpha actin promoter, troponin 1 promoter, Na^+/Ca^{2+} exchanger promoter, dystrophin promoter, creatine kinase promoter, alpha7 integrin promoter, brain natriuretic peptide promoter, or alpha B-crystallin/small heat shock protein promoter, alpha myosin heavy chain promoter, or atrial natriuretic

20   factor promoter. Alternatively, the promoter may be the native MCIP1 promoter. The nucleic acid may further comprise an origin of replication. The nucleic acid may a non-viral vector or a viral vector.

In still another aspect of the invention, there is provided an isolated and purified nucleic acid encoding an MCIP1 polypeptide lacking residues 1-80 of SEQ ID NO:2,

25   optionally, comprising a promoter. In a related aspect of the invention, there is provided an isolated and purified MCIP1 polypeptide lacking amino acid residues corresponding to Exons 1, 2 and 3. In another related asepct of the invention, there is provided an isolated and purified MCIP1 polypeptide lacking residues 1-80 of SEQ ID NO:2.

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BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

FIGS. 1A-B - MCIP1 inhibits calcineurin-dependent transcriptional responses in C2C12 myogenic cells. Luciferase reporter constructs under the control of a minimal promoter (TATA-luc) or promoter/enhancer elements from the myoglobin (Mb-luc) or interleukin-2 (IL-2-luc) genes were cotransfected into C2C12 cells along with expression plasmids containing either no insert (pCI), or CnA*, or MCIP1. Data are expressed relative to the luciferase activity observed in the control state (pCI) and represent mean values (± S.E.) of duplicate determinations from three or more independent experiments. All results are corrected for variations in transfection efficiency by normalization to expression of a co-transfected pCMV-lacZ plasmid. FIG. 1A: myoblasts harvested 24 h after transfection or myotubes harvested 72 h after transfection. FIG. 1B: myotubes harvested 72 h after cotransfection with a luciferase reporter under the control of three copies of a Gal4p binding site (UASg-TATA-luc), and plasmids encoding Gal4-VP16 fusion protein or MCIP1.

FIGS. 2A-C - The inhibitory effect of MCIP1 is on calcineurin itself rather than on downstream effectors of calcineurin signaling. FIG. 2A: MCIP1 inhibits the transcriptional response to activation of endogenous calcineurin. C2C12 cells were transfected with the Mb-luc reporter plus or minus MCIP1. The transfected cells were stimulated with 1 μM ionomycin and 10 ng/ml PMA 4.5 h prior to harvesting. Data were calculated as described in FIGS. 1A-B. FIG. 2B: MCIP1 fails to inhibit the transcriptional response to a constitutively active (calcineurin-independent) form of NFATc. C2C12 cells were cotransfected with the IL-2-luc reporter and plasmids encoding MCIP or a constitutively active form of NFATc

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(NFAT) as indicated. Cells were harvested 24 h after transfection. FIG. 2C: MCIP1 inhibits calcineurin-dependent stimulation of the transactivating function of MEF2. C2C12 cells were transfected with a luciferase reporter containing three copies of a high affinity MEF2 binding site from the desmin gene (des-MEF2-luc). The reporter was stimulated by cotransfection with plasmids encoding constitutively active forms of calcineurin (CnA*), calmodulin-dependent protein kinase IV (CaMKIV) and MCIP1 as indicated. Cells were harvested 48 h after transfection. All results are corrected for variations in transfection efficiency by normalization to expression of a co-transfected pCMV-lacZ plasmid.

FIG. 3 - Splice variants of MCIP1 and MCIP2 inhibit calcineurin signaling. C2C12 cells were cotransfected with the Mb-luc reporter plasmid, an empty control vector (pCI), or expression vectors encoding constitutively active calcineurin (CnA*), human MCIP1 (hMCIP1), two splice variants of murine MCIP1 (mMCIP1/exon 1 or mMCIP1/exon4), or murine MCIP2 (mMCIP2) as indicated. Cells were harvested 48 h after transfection. Luciferase expression was determined in the absence (open bar) or presence (filled bars) of constitutively active calcineurin (CnA*). Data were calculated as described in FIGS. 1A-B. All results are corrected for variations in transfection efficiency by normalization to expression of a co-transfected pCMV-lacZ plasmid.

FIGS. 4A-B - MCIP1 binds the catalytic domain of calcineurin A. FIG. 4A: schematic depiction of functional domains of calcineurin A, as defined by previous studies (1), and including the catalytic domain, binding sites for calcineurin B (B) and calmodulin (M), and the carboxyl-terminal autoinhibitory domain (I). Truncated forms of calcineurin A are identified by their termination at specific amino acid (aa) residues corresponding to positions within the full-length protein, and by their binding to MCIP1. FIG. 4B: calcineurin A proteins were translated in rabbit reticulocyte lysates and labeled with [^{35}S]methionine. Recombinant GST-MCIP1 was purified from bacteria and coupled to glutathione-agarose beads. Binding of truncated forms of calcineurin A to GST-MCIP1 was

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compared with GST alone, and to 25% of the total pool of metabolically labeled protein included in the binding reaction (Input). Luciferase failed to interact with GST-MCIP1, serving as a negative control (data not shown). Proteins were separated by SDS-PAGE and visualized by autoradiography.

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FIGS. 5A-B - Conserved regions of MCIP1 mediate the interaction with calcineurin A. FIG. 5A: schematic depiction of MCIP1 illustrating amino acid sequence motifs conserved with yeast Rex1p (24) and mammalian NFAT (3) proteins, and including an SP repeat region and calcineurin docking motif (P).

10 Truncated forms of MCIP1 are identified by their termination at specific amino acid (aa) residues corresponding to positions within the full-length protein, and by their binding to calcineurin A. FIG. 5B: calcineurin A (amino acids 1-398) was translated in rabbit reticulocyte lysates and labeled with $[^{35}S]$methionine. Recombinant full-length or truncated forms of GST-MCIP1 were purified from

15 bacteria and coupled to glutathione-agarose beads. Binding of calcineurin A to each variant of GST-MCIP1 was compared with GST alone, and to 25% of the total pool of metabolically labeled protein included in the binding reaction (input). Proteins were separated by SDS-PAGE and visualized by autoradiography.

20 **FIGS. 6A-B** - Muscle-selective expression of MCIP1 and MCIP2 mRNA. FIG. 6A: Northern blots demonstrating expression of a 2.2-kB pair MCIP1 transcript, and two MCIP2 transcripts of 3.4 and 1.4 kB pairs in tissues of adult mice. Both genes are more highly expressed in heart and soleus skeletal muscles than in other tissues, with the exception that MCIP2 transcripts are also abundant in brain. Each

25 lane was loaded with 20 μg of total RNA, and equivalent loading was confirmed by ethidium bromide staining. FIG. 6B: Northern blot demonstrating increased expression of MCIP1 during differentiation of C2C12 myogenic cells in culture.

FIG. 7 - Gene expression profiling by microarray analysis (Incyte Genomics).

30 Listed are the eight genes found to be potently up-regulated during compensated hypertrophy (upper panel) and in the transition to overt heart failure (lower panel)

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that are characteristic of this model (3), along with accession numbers and estimated fold-change in mRNA abundance. Calcineurin A is the transgene product in this model and up-regulation of atrial natriuretic factor gene expression is a well-defined marker of cardiac hypertrophy. MCIP1 (arrows) is one of the genes most strongly activated in hypertrophic, non-failing hearts of aMHC-CnA* animals, and is up-regulated further in hearts of animals that have progressed to overt cardiac failure.

FIGS. 8A-C - An intragenic calcineurin response element from the MCIP1 gene. FIG. 8A. Schematic representation of the organization of the human MCIP1 (DSCR1) gene, indicating four alternative initial exons (E1-E4) and three exons common to all forms of MCIP1 mRNA (E5-E7)34. The nucleotide sequence flanking Exon 4 is shown to illustrate the presence of 15 consensus binding sites for NF-AT transcription factors (boxes). The first nucleotide of exon 4 is designated as +1. FIG. 8B. MCIP1-luciferase reporter plasmids. Plasmids were constructed to link defined genomic segments proximal to exon 4 of the human MCIP1 gene to a luciferase reporter gene. The numbers of NF-AT consensus binding sites contained within each segment are shown in parenthesis. FIG. 8D. Transient transfection assays of MCIP1-luciferase reporter plasmids. Results were corrected for variations in transfection efficiency by normalization to expression of a co-transfected pCMV-lacZ plasmid. Fold activation was determined relative to the basal activity of the *874 to +30 MCIP1-luciferase reporter construct. Histograms represent mean values + SEM of 3 independent transfections of C2C12 myogenic cells.

FIG. 9 - A negative feedback loop for regulation of calcineurin activity. Evidence presented in this paper identifies MCIP1 as a target for positive transcriptional regulation by calcineurin in heart and skeletal muscles, probably as a direct consequence of NF-AT binding to a calcineurin responsive region in proximity to exon 4 of the MCIP1 gene. Since MCIP1 is capable of inhibiting the enzymatic activity of calcineurin (24), it is likely that this regulatory circuit serves

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to inhibit calcineurin activity under conditions of sustained stimulation by calcium/calmodulin, thereby to protect cells from deleterious effects of unrestrained calcineurin activation.

FIG. 10 - <u>Design and expression of the α-MHC-hMCIP1 transgene</u>. Schematic illustration of components of the transgene, including a 5.5 kb α-MHC promoter fragment with three non-coding exons (E1, E2, E3) and intervening non-transcribed segments of the α-MHC gene, followed by a full length human MCIP1 cDNA with a carboxyl terminal epitope tag (HA) and a polyadenylation (pA) signal from the human growth hormone gene. The lower line illustrates the unexpected pattern of mRNA splicing observed *in vivo*, resulting in translation of a truncated protein (DhMICP1) initiated at amino acid 81 relative to the wild-type (WT) protein.

FIG. 11 - <u>Functional activity of the truncated DhMCIP1 protein product compared to full length hMCIP1, assessed by inhibition of calcineurin-dependent activation in C2C12 myoblasts</u>. C2C12 cells were transfected with a luciferase reporter gene driven by a calcineurin-responsive IL-2 promoter (IL-2-Luc). Cells were cotransfected with a constitutively active calcineurin expression plasmid (pCMV-CnA*) and either an empty control vector (pCMV-neo) or the indicated MCIP encoding plasmid (pCMV-hMCIP1 or pCMV-ΔhMCIP1).

FIG. 12 - <u>Effects of hMCIP1 on cardiac hypertrophy in response to b-adrenergic receptor stimulation or exercise in intact animals</u>. The graph indicates the percent increase in htw/bw of male wild-type (n=7) and α-MHC-hMCIP1 transgenic (n=9) mice subjected to chronic infusion of isoproterenol over seven days or the percent increase in htw/bw of male wil- type (n=4) and α-MHC-hMCIP1 transgenic (n=4) mice after 28 days of voluntary wheel running exercise. The α-MHC-hMCIP1 mice developed significantly less cardiac hypertrophy in response to either isoproterenol or exercise.

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DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

Heart failure – the inability of the heart to pump blood at a rate sufficient to sustain homeostasis – is a major health issue in the world today. This is true not only due to the untimely deaths caused by heart disease, but the tremendous expense incurred due to required patient support, including prolonged hospitalization. Thus, there remains a great need to address this costly and debilitating disease.

The present inventors now report that the mammalian MCIPs (myocyte-enriched calcineurin interacting proteins) are capable of binding and inhibiting the catalytic subunit of calcineurin. MCIP proteins are structurally distinct from immunophilins, AKAP79 and cabin-1/cain proteins that have been shown previously to modulate the signaling function of calcineurin. Moreover, MCIPs are expressed most abundantly in striated myocytes of the heart and skeletal muscles, a pattern that is unique among this set of known calcineurin-interacting proteins.

In particular, cabin-1/cain is expressed at lower levels in striated muscles than in other tissues (Sun *et al.*, 1998; Lai *et al.*, 1998). AKAP79 and cabin-1/cain are larger proteins that appear to function as molecular scaffolds upon which hetero-oligomeric complexes that include calcineurin are assembled (Sun *et al.*, 1998; Lai *et al.*, 1998; Klauck *et al.*, 1996). The contrastingly small size (22 kDa) of MCIPs suggests a different mechanism of action.

As discussed above, Rex1p (YKL159c) is a calcineurin-binding protein of *Saccharomyces cerevisiae*. A preliminary report noted that this small 24 kDa protein inhibited calcineurin signaling when overexpressed in yeast (Kingsbury and Cunningham 1998). A 30-amino acid segment of Rex1p shares homology to two different genes identified in the human gene sequence data base, DSCR1 and ZAKI-4. DSCR1 was so designated because it resides within the "Down syndrome critical region" of human chromosome 21 (Fuentes *et al.*, 1997). Individuals trisomic for this region, which is estimated to encode 50-100 different proteins, display features of the Down syndrome

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phenotype. ZAKI-4 was identified from a human fibroblast cell line in a screen for genes that are transcriptionally activated in response to thyroid hormone (Miyazaki *et al.*, 1996).

5   The inventors were stimulated by these observations and undertook a detailed analysis of the proteins encoded by these genes with respect to calcineurin signaling in mammalian cells. Based on these studies, DSCR1 (MCIP1) and ZAKI-4 (MCIP2) genes are capable of inhibiting calcineurin-dependent transcriptional responses in murine myocytes. MCIPs represent unique targets for efforts to regulate calcineurin signaling

10   selectively in cardiac and skeletal myocytes.

       MCIP proteins exhibit structural motifs that are shared both with Rex1p and with NFAT, the most intensively characterized phosphoprotein substrate for calcineurin. These conserved motifs within MCIP appear to have functional importance, since

15   truncated forms of MCIP1 from which these regions have been removed are defective for binding calcineurin. MCIP1 binds within the catalytic domain of calcineurin A that is discrete from the carboxyl-terminal region required for binding of calmodulin. This result suggests that MCIP1 may contact the active site of calcineurin, perhaps functioning to inhibit access of NFAT and other phosphoprotein substrates.

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       MCIP1 transcripts are increased several-fold in hearts of transgenic mice overexpressing a constitutively active form of calcineurin under the control of a cardiac-specific promoter. Microarray analysis of these hearts, compared to wild-type, ranks MCIP1 as the single gene that is most dramatically upregulated. In contrast, MCIP2

25   transcription does not change in response to increases in calcineurin activity, suggesting that MCIP1, but not MCIP2, functions in a negative feedback loop in response to calcineurin activity. However, MCIP2 is upregulated by thyroid hormone.

       Since transcription of MCIP1 is regulated so potently by calcineurin activity, the

30   MCIP1 gene promoter becomes a valuable reagent for high throughput drug screens to identify compounds that alter calcineurin signalling. An 700 bp intragenic segment of the

MCIP1 gene contains a uniquely dense cluster of 15 NFAT binding elements immediately upstream (5') to Exon 4, and the form of MCIP1 induced by calcineurin is initiated from Exon 4. This genomic organization is likely to provide the basis for the exquisite sensitivity of MCIP1 transcription to calcineurin activity. Transcription of

5   MCIP1 also is responsive to oxidative stress, peaking around four hours after stimulation. MCIP2 levels do not change at four hours, but decline as MCIP1 levels peak.

In particular, the inventors have identified a phosphoserine residue at amino acid 108 of MCIP1 as a substrate for calcineurin phosphatase activity. A priming

10   phosphorylation of a serine at amino acid 112 of MCIP1 by a mitogen activited protein kinase (MAPK) is required for subsequent phosphorylation of serine 108 by glyogen synthase kinsase-3 (GSK3). Calcineurin can dephosphorylate serine 108, but not remove the phosphate at serine 112. However, a mutant MCIP1 with serine 108 converted to alanine still inhibits calcineurin.

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Recently, additions to the human genome data base includes a third MCIP gene, with two splice variants. This gene is located on chromosome 1, with the variants having accession numbers AF176116 (SEQ ID NOS:16 and 17) and AF176117 (SEQ ID NOS:5 and 6). These gene products are termed MCIP3a and MCIP3b by the inventors. There

20   also appears to be a splice variant of MCIP2, now called MCIP2a and MCIP2b.

The discovery of proteins that function to regulate calcineurin-dependent signaling cascades is important, both for advancing the basic understanding of cell regulation and to provide novel targets for drug discovery. The ability of MCIPs to

25   inhibit calcineurin activity potentially adds a level of complexity to the regulation of calcineurin signaling in those cell types in which MCIP proteins are expressed. MCIPs themselves may be subject to regulation by protein phosphorylation and dephosphorylation, and thereby may serve to integrate other signaling inputs with the calcineurin pathway. The inventors speculate that these proteins serve as negative

30   regulators to prevent adverse consequences of unrestrained calcineurin activity in muscle tissues (Molkentin et al., Musaro et al., 1999; Semsarian et al., 1999; Dunn et al., 1999).

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However, it also is possible that the interaction with MCIP directs calcineurin to specific intracellular locales or to specific phosphoprotein substrates.

Current results indicate that the interaction between MCIP and calcineurin is pertinent to the pathobiology, and ultimately to the therapy, of human disease. For example, familial forms of hypertrophic cardiomyopathy are caused by mutations in genes encoding proteins of the sarcomere (Seidman and Seidman, 1998), in a manner that is likely to involve calcineurin signaling (Marban *et al.*, 1987). Administration of the calcineurin antagonist drugs cyclosporin A or FK-506 prevents cardiac hypertrophy in transgenic animal models of familial forms of hypertrophic cardiomyopathy (Sussman *et al.*, 1998), but the analogous clinical trials are precluded because of toxic side effects (*e.g.*, immunosuppression and hypertension) of existing agents.

It also is possible, in some clinical situations, that faciliation of cardiac hypertrophy without other aspects of the disease could prove beneficial. Again, MCIP's involvement in this process makes it a suitable candidate for intervention, this time by antagonizing MCIP rather than calcineurin.

Calcineurin antagonists also prevent cardiac hypertrophy and heart failure in some, although not all, animal models of acquired forms of cardiomyopathy that are common in human populations (Sussman *et al.*, 1998; Ding *et al.*, 1999; Zhang *et al.*, 1999), but the same limitations to clinical trials apply. The relative abundance of MCIP1 in cardiac muscle recommends it as a target for drug development to circumvent these limitations of current calcineurin antagonists.

I.   MCIP Peptides and Polypeptides

The human gene (DSCR1) encoding MCIP1 is one of 50-100 genes that reside within a critical region of chromosome 21 (Fuentes *et al.*, 1997; Fuentes *et al.*, 1995), trisomy of which gives rise to the complex developmental abnormalities of Down syndrome, which include cardiac abnormalities and skeletal muscle hypotonia as prominent features (Epstein, 1995). ZAKI-4 was identified from a human fibroblast cell

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line in a screen for genes that are transcriptionally activated in response to thyroid hormone (Miyazaki *et al.*, 1996).

Applicants provide protein sequences for human MCIP1, MCIP2 and MCIP3 (SEQ ID NOS:2, 4, 6 and 17) and mouse MCIP1 and MCIP2 (SEQ ID NOS:8 and 10). In addition to the entire MCIP1, MCIP2 and MCIP3 molecules, the present invention also relates to fragments of the polypeptides that may or may not retain various of the functions described below. Fragments, including the N-terminus of the molecule may be generated by genetic engineering of translation stop sites within the coding region (discussed below). Alternatively, treatment of the MCIPs with proteolytic enzymes, known as proteases, can produces a variety of N-terminal, C-terminal and internal fragments. Examples of fragments may include contiguous residues of SEQ ID NOS:2, 4, 6, 8, 10 and 17 of 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 55, 60, 65, 75, 80, 85, 90, 95, 100, 200, 300, 400 or more amino acids in length. These fragments may be purified according to known methods, such as precipitation (*e.g.*, ammonium sulfate), HPLC, ion exchange chromatography, affinity chromatography (including immunoaffinity chromatography) or various size separations (sedimentation, gel electrophoresis, gel filtration).

A.   Structural Features

MCIP1 is the product of a human gene previously called DSCR1, and it includes several domains of proven or potential biological interest: an acidic domain (EKEEEEME), a serine-proline motif (SPPASPP), a leucine-rich putative DNA binding domain (LHKTEFLGKEMKLYFAQTL), and regions with the characteristics of an SH3 or SH2 domain ligand (HLAPPNPDK and PEYTPI, respectively). Fuentes *et al.* (1997). Multiple versions of MCIP1 exist due to four alternative first exons, which are alternatively joined to Exons 5-7. It is the form of MCIP1 initiated at Exon 4 that is transcriptionally induced by calcineurin activity. MCIP2, also known as ZAKI-4, is a 192 AA polypeptide having 62% homology with MCIP1. Proline and valine residues are found with abundance within MCIP2. Miyazaki *et al.* (1996).

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B. Functional Aspects

MCIP1 is a binding partner for calcineurin. In addition, it is an antagonist of calcineurin-dependent transcriptional activation. MCIP1 also acts as a substrate for phosphoryalation by MAPK and GSK-3, and calcineurin's phosphatase activity. Residues 81-177 of MCIP1 retain the calcineurin inhibitory action.

Binding of MCIP1 to calcineurin does not require calmodulin, nor does MCIP interfere with calmodulin binding to calcineurin. This suggests that the surface of calcineurin to which MCIP1 bindings does not include the calmodulin binding domain. In contrast, the interaction of MCIP1 with calcineurin is disrupted by FK506:FKBP or cyclosporin:cyclophylin, indicating that the surface of calcineurin to which MCIP1 binds overlaps with that required for the activity of immunosuppressive drugs.

C. Variants of MCIP1 and MCIP2

Amino acid sequence variants of the polypeptide can be substitutional, insertional or deletion variants. Deletion variants lack one or more residues of the native protein which are not essential for function or immunogenic activity, and are exemplified by the variants lacking a transmembrane sequence described above. Another common type of deletion variant is one lacking secretory signal sequences or signal sequences directing a protein to bind to a particular part of a cell. Insertional mutants typically involve the addition of material at a non-terminal point in the polypeptide. This may include the insertion of an immunoreactive epitope or simply a single residue. Terminal additions, called fusion proteins, are discussed below.

Substitutional variants typically contain the exchange of one amino acid for another at one or more sites within the protein, and may be designed to modulate one or more properties of the polypeptide, such as stability against proteolytic cleavage, without the loss of other functions or properties. Substitutions of this kind preferably are conservative, that is, one amino acid is replaced with one of similar shape and charge. Conservative substitutions are well known in the art and include, for example, the changes of: alanine to serine; arginine to lysine; asparagine to glutamine or histidine; aspartate to glutamate;

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cysteine to serine; glutamine to asparagine; glutamate to aspartate; glycine to proline; histidine to asparagine or glutamine; isoleucine to leucine or valine; leucine to valine or isoleucine; lysine to arginine; methionine to leucine or isoleucine; phenylalanine to tyrosine, leucine or methionine; serine to threonine; threonine to serine; tryptophan to tyrosine; tyrosine to tryptophan or phenylalanine; and valine to isoleucine or leucine.

The following is a discussion based upon changing of the amino acids of a protein to create an equivalent, or even an improved, second-generation molecule. For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid substitutions can be made in a protein sequence, and its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the DNA sequences of genes without appreciable loss of their biological utility or activity, as discussed below. Table 1 shows the codons that encode particular amino acids.

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like.

Each amino acid has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics (Kyte and Doolittle, 1982), these are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8);

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tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.*, still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those which are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein. As detailed in U.S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 ± 1); alanine (-0.5); histidine *-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4).

It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent and immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those that are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that take various of the foregoing characteristics into consideration are well known to those of skill in the art and

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include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

Another embodiment for the preparation of polypeptides according to the invention is the use of peptide mimetics. Mimetics are peptide-containing molecules that mimic elements of protein secondary structure (Johnson *et al,* 1993). The underlying rationale behind the use of peptide mimetics is that the peptide backbone of proteins exists chiefly to orient amino acid side chains in such a way as to facilitate molecular interactions, such as those of antibody and antigen. A peptide mimetic is expected to permit molecular interactions similar to the natural molecule. These principles may be used, in conjunction with the principles outline above, to engineer second generation molecules having many of the natural properties of MCIP1, MCIP2 and MCIP3, but with altered and even improved characteristics.

D. Domain Switching

As described in the examples, the present inventors have identified murine MCIP1, MCIP2 and MCIP3. Given the homology with other Midline proteins, an interesting series of mutants can be created by substituting homologous regions of various proteins. This is known, in certain contexts, as "domain switching."

Domain switching involves the generation of chimeric molecules using different but, in this case, related polypeptides. By comparing various MCIP proteins, one can make predictions as to the functionally significant regions of these molecules. It is possible, then, to switch related domains of these molecules in an effort to determine the criticality of these regions to MCIP1, MCIP2 and MCIP3 function. These molecules may have additional value in that these "chimeras" can be distinguished from natural molecules, while possibly providing the same function.

E. Fusion Proteins

A specialized kind of insertional variant is the fusion protein. This molecule generally has all or a substantial portion of the native molecule, linked at the N- or C-
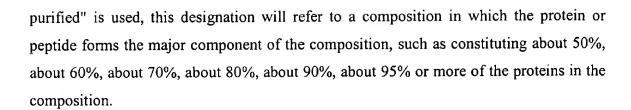
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terminus, to all or a portion of a second polypeptide. For example, fusions typically employ leader sequences from other species to permit the recombinant expression of a protein in a heterologous host. Another useful fusion includes the addition of a immunologically active domain, such as an antibody epitope, to facilitate purification of the fusion protein.

5   Inclusion of a cleavage site at or near the fusion junction will facilitate removal of the extraneous polypeptide after purification. Other useful fusions include linking of functional domains, such as active sites from enzymes, glycosylation domains, cellular targeting signals or transmembrane regions.

10   *F.   Purification of Proteins*

It will be desirable to purify MCIP1, MCIP2, MCIP3 or variants thereof. Protein purification techniques are well known to those of skill in the art. These techniques involve, at one level, the crude fractionation of the cellular milieu to polypeptide and non-polypeptide fractions. Having separated the polypeptide from other proteins, the

15   polypeptide of interest may be further purified using chromatographic and electrophoretic techniques to achieve partial or complete purification (or purification to homogeneity). Analytical methods particularly suited to the preparation of a pure peptide are ion-exchange chromatography, exclusion chromatography; polyacrylamide gel electrophoresis; isoelectric focusing. A particularly efficient method of purifying

20   peptides is fast protein liquid chromatography or even HPLC.

Certain aspects of the present invention concern the purification, and in particular embodiments, the substantial purification, of an encoded protein or peptide. The term "purified protein or peptide" as used herein, is intended to refer to a composition,

25   isolatable from other components, wherein the protein or peptide is purified to any degree relative to its naturally-obtainable state. A purified protein or peptide therefore also refers to a protein or peptide, free from the environment in which it may naturally occur.

Generally, "purified" will refer to a protein or peptide composition that has been

30   subjected to fractionation to remove various other components, and which composition substantially retains its expressed biological activity. Where the term "substantially

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purified" is used, this designation will refer to a composition in which the protein or peptide forms the major component of the composition, such as constituting about 50%, about 60%, about 70%, about 80%, about 90%, about 95% or more of the proteins in the composition.

Various methods for quantifying the degree of purification of the protein or peptide will be known to those of skill in the art in light of the present disclosure. These include, for example, determining the specific activity of an active fraction, or assessing the amount of polypeptides within a fraction by SDS/PAGE analysis. A preferred method for assessing the purity of a fraction is to calculate the specific activity of the fraction, to compare it to the specific activity of the initial extract, and to thus calculate the degree of purity, herein assessed by a "-fold purification number." The actual units used to represent the amount of activity will, of course, be dependent upon the particular assay technique chosen to follow the purification and whether or not the expressed protein or peptide exhibits a detectable activity.

Various techniques suitable for use in protein purification will be well known to those of skill in the art. These include, for example, precipitation with ammonium sulphate, PEG, antibodies and the like or by heat denaturation, followed by centrifugation; chromatography steps such as ion exchange, gel filtration, reverse phase, hydroxylapatite and affinity chromatography; isoelectric focusing; gel electrophoresis; and combinations of such and other techniques. As is generally known in the art, it is believed that the order of conducting the various purification steps may be changed, or that certain steps may be omitted, and still result in a suitable method for the preparation of a substantially purified protein or peptide.

There is no general requirement that the protein or peptide always be provided in their most purified state. Indeed, it is contemplated that less substantially purified products will have utility in certain embodiments. Partial purification may be accomplished by using fewer purification steps in combination, or by utilizing different forms of the same general purification scheme. For example, it is appreciated that a

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cation-exchange column chromatography performed utilizing an HPLC apparatus will generally result in a greater "-fold" purification than the same technique utilizing a low pressure chromatography system.   Methods exhibiting a lower degree of relative purification may have advantages in total recovery of protein product, or in maintaining

5   the activity of an expressed protein.

It is known that the migration of a polypeptide can vary, sometimes significantly, with different conditions of SDS/PAGE (Capaldi *et al.*, 1977). It will therefore be appreciated that under differing electrophoresis conditions, the apparent molecular

10   weights of purified or partially purified expression products may vary.

High Performance Liquid Chromatography (HPLC) is characterized by a very rapid separation with extraordinary resolution of peaks. This is achieved by the use of very fine particles and high pressure to maintain an adequate flow rate. Separation can be

15   accomplished in a matter of minutes, or at most an hour. Moreover, only a very small volume of the sample is needed because the particles are so small and close-packed that the void volume is a very small fraction of the bed volume. Also, the concentration of the sample need not be very great because the bands are so narrow that there is very little dilution of the sample.

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Gel chromatography, or molecular sieve chromatography, is a special type of partition chromatography that is based on molecular size.   The theory behind gel chromatography is that the column, which is prepared with tiny particles of an inert substance that contain small pores, separates larger molecules from smaller molecules as

25   they pass through or around the pores, depending on their size. As long as the material of which the particles are made does not adsorb the molecules, the sole factor determining rate of flow is the size. Hence, molecules are eluted from the column in decreasing size, so long as the shape is relatively constant. Gel chromatography is unsurpassed for separating molecules of different size because separation is independent of all other

30   factors such as pH, ionic strength, temperature, etc. There also is virtually no adsorption,

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less zone spreading and the elution volume is related in a simple matter to molecular weight.

Affinity Chromatography is a chromatographic procedure that relies on the
5   specific affinity between a substance to be isolated and a molecule that it can specifically bind to. This is a receptor-ligand type interaction. The column material is synthesized by covalently coupling one of the binding partners to an insoluble matrix. The column material is then able to specifically adsorb the substance from the solution. Elution occurs by changing the conditions to those in which binding will not occur (alter pH,
10   ionic strength, temperature, *etc.*).

A particular type of affinity chromatography useful in the purification of carbohydrate containing compounds is lectin affinity chromatography. Lectins are a class of substances that bind to a variety of polysaccharides and glycoproteins. Lectins are
15   usually coupled to agarose by cyanogen bromide. Conconavalin A coupled to Sepharose was the first material of this sort to be used and has been widely used in the isolation of polysaccharides and glycoproteins other lectins that have been include lentil lectin, wheat germ agglutinin which has been useful in the purification of N-acetyl glucosaminyl residues and *Helix pomatia* lectin. Lectins themselves are purified using affinity
20   chromatography with carbohydrate ligands. Lactose has been used to purify lectins from castor bean and peanuts; maltose has been useful in extracting lectins from lentils and jack bean; N-acetyl-D galactosamine is used for purifying lectins from soybean; N-acetyl glucosaminyl binds to lectins from wheat germ; D-galactosamine has been used in obtaining lectins from clams and L-fucose will bind to lectins from lotus.

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The matrix should be a substance that itself does not adsorb molecules to any significant extent and that has a broad range of chemical, physical and thermal stability. The ligand should be coupled in such a way as to not affect its binding properties. The ligand should also provide relatively tight binding. And it should be possible to elute the
30   substance without destroying the sample or the ligand. One of the most common forms of affinity chromatography is immunoaffinity chromatography. The generation of

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antibodies that would be suitable for use in accord with the present invention is discussed below.

G.   *Synthetic Peptides*

5   The present invention also describes smaller MCIP-related peptides for use in various embodiments of the present invention. Because of their relatively small size, the peptides of the invention can also be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. See, for

10   example, Stewart and Young, (1984); Tam *et al.*, (1983); Merrifield, (1986); and Barany and Merrifield (1979), each incorporated herein by reference. Short peptide sequences, or libraries of overlapping peptides, usually from about 6 up to about 35 to 50 amino acids, which correspond to the selected regions described herein, can be readily synthesized and then screened in screening assays designed to identify reactive peptides.

15   Alternatively, recombinant DNA technology may be employed wherein a nucleotide sequence which encodes a peptide of the invention is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression.

20   ### H.   *Antigen Compositions*

The present invention also provides for the use of MCIP1, MCIP2 and MCIP3 proteins or peptides as antigens for the immunization of animals relating to the production of antibodies. It is envisioned that MCIP1, MCIP2, MCIP3 or portions thereof, will be coupled, bonded, bound, conjugated or chemically-linked to one or more

25   agents via linkers, polylinkers or derivatized amino acids. This may be performed such that a bispecific or multivalent composition or vaccine is produced. It is further envisioned that the methods used in the preparation of these compositions will be familiar to those of skill in the art and should be suitable for administration to animals, *i.e.*, pharmaceutically acceptable. Preferred agents are the carriers are keyhole limpet

30   hemocyannin (KLH) or bovine serum albumin (BSA).

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II.   Nucleic Acids

The present invention also provides, in another embodiment, genes encoding MCIP1 and MCIP2. Genes for human MCIP1 (SEQ ID NO:1), MCIP2 (SEQ ID NO:3) and MCIP3 (SEQ ID:5 and 16) have been identified. Also provided are MCIP1 and

5 MCIP2 from mouse (SEQ ID NOS:7 and 9). The present invention is not limited in scope to these genes, however, as one of ordinary skill in the could, using these nucleic acids, readily identify related homologs in various other species (e.g., rat, rabbit, dog, monkey, gibbon, human, chimp, ape, baboon, cow, pig, horse, sheep, cat and other species).

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In addition, it should be clear that the present invention is not limited to the specific nucleic acids disclosed herein. As discussed below, an "MCIP gene" may contain a variety of different bases and yet still produce a corresponding polypeptide that is functionally indistinguishable, and in some cases structurally, from the human and

15 mouse genes disclosed herein.

Similarly, any reference to a nucleic acid should be read as encompassing a host cell containing that nucleic acid and, in some cases, capable of expressing the product of that nucleic acid. In addition to therapeutic considerations, cells expressing nucleic acids

20 of the present invention may prove useful in the context of screening for agents that induce, repress, inhibit, augment, interfere with, block, abrogate, stimulate or enhance the function of MCIP1, MCIP2 or MCIP3.

A.   Nucleic Acids Encoding MCIP1, MCIP2 and MCIP3

25 Nucleic acids according to the present invention may encode an entire MCIP1, MCIP2 or MCIP3 gene, a domain of MCIP1, MCIP2 or MCIP3, or any other fragment of MCIP1, MCIP2 and MCIP3 as set forth herein. The nucleic acid may be derived from genomic DNA, i.e., cloned directly from the genome of a particular organism. In preferred embodiments, however, the nucleic acid would comprise complementary DNA (cDNA).

30 Also contemplated is a cDNA plus a natural intron or an intron derived from another gene; such engineered molecules are sometime referred to as "mini-genes." At a minimum, these

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and other nucleic acids of the present invention may be used as molecular weight standards in, for example, gel electrophoresis.

The term "cDNA" is intended to refer to DNA prepared using messenger RNA (mRNA) as template. The advantage of using a cDNA, as opposed to genomic DNA or DNA polymerized from a genomic, non- or partially-processed RNA template, is that the cDNA primarily contains coding sequences of the corresponding protein. There may be times when the full or partial genomic sequence is preferred, such as where the non-coding regions are required for optimal expression or where non-coding regions such as introns are to be targeted in an antisense strategy.

It also is contemplated that a given MCIP from a given species may be represented by natural variants that have slightly different nucleic acid sequences but, nonetheless, encode the same protein (see Table 1 below).

~~As used in this application, the term "a nucleic acid encoding a MCIP" refers to a~~ nucleic acid molecule that has been isolated free of total cellular nucleic acid. In preferred embodiments, the invention concerns a nucleic acid sequence essentially as set forth in SEQ ID NOS: 1, 3, 5, 7. 9 and 16. The term "as set forth in SEQ ID NOS: 1, 3, 5, 7, 9 or 16" means that the nucleic acid sequence substantially corresponds to a portion of SEQ ID NO:1, 3, 5, 7, 9 or 16. The term "functionally equivalent codon" is used herein to refer to codons that encode the same amino acid, such as the six codons for arginine or serine (Table 1, below), and also refers to codons that encode biologically equivalent amino acids, as ~~discussed in the following pages.~~

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TABLE 1

Amino Acids			Codons					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	UGC	UGU				
Aspartic acid	Asp	D	GAC	GAU				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	UUC	UUU				
Glycine	Gly	G	GGA	GGC	GGG	GGU		
Histidine	His	H	CAC	CAU				
Isoleucine	Ile	I	AUA	AUC	AUU			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU
Methionine	Met	M	AUG					
Asparagine	Asn	N	AAC	AAU				
Proline	Pro	P	CCA	CCC	CCG	CCU		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
Threonine	Thr	T	ACA	ACC	ACG	ACU		
Valine	Val	V	GUA	GUC	GUG	GUU		
Tryptophan	Trp	W	UGG					
Tyrosine	Tyr	Y	UAC	UAU				

Allowing for the degeneracy of the genetic code, sequences that have at least about 50%,
5 usually at least about 60%, more usually about 70%, most usually about 80%, preferably at least about 90% and most preferably about 95% of nucleotides that are identical to the nucleotides of SEQ ID NOS:1, 3, 5, 7, 9 and 16 are contemplated. Sequences that are essentially the same as those set forth in SEQ ID NOS:1, 3, 5, 7, 9 and 16 also may be functionally defined as sequences that are capable of hybridizing to a nucleic acid segment
10 containing the complement of SEQ ID NOS:1, 3, 5, 7, 9 and 16 under standard conditions.

The DNA segments of the present invention include those encoding biologically functional equivalent MCIP proteins and peptides, as described above. Such sequences may arise as a consequence of codon redundancy and amino acid functional equivalency that are
15 known to occur naturally within nucleic acid sequences and the proteins thus encoded. Alternatively, functionally equivalent proteins or peptides may be created via the application of recombinant DNA technology, in which changes in the protein structure may be engineered, based on considerations of the properties of the amino acids being exchanged.

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Changes designed by man may be introduced through the application of site-directed mutagenesis techniques or may be introduced randomly and screened later for the desired function, as described below.

5   *B.   Oligonucleotide Probes and Primers*

Naturally, the present invention also encompasses DNA segments that are complementary, or essentially complementary, to the sequence set forth in SEQ ID NOS:1, 3, 5, 7, 9 and 16. Nucleic acid sequences that are "complementary" are those that are capable of base-pairing according to the standard Watson-Crick complementary rules. As

10   used herein, the term "complementary sequences" means nucleic acid sequences that are substantially complementary, as may be assessed by the same nucleotide comparison set forth above, or as defined as being capable of hybridizing to the nucleic acid segment of SEQ ID NOS:1, 3, 5, 7, 9 and 16 under relatively stringent conditions such as those described herein. Such sequences may encode the entire MCIP proteins or functional or

15   non-functional fragments thereof.

Alternatively, the hybridizing segments may be shorter oligonucleotides. Sequences of 17 bases long should occur only once in the human genome and, therefore, suffice to specify a unique target sequence. Although shorter oligomers are easier to make and

20   increase *in vivo* accessibility, numerous other factors are involved in determining the specificity of hybridization. Both binding affinity and sequence specificity of an oligonucleotide to its complementary target increases with increasing length. It is contemplated that exemplary oligonucleotides of 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more base pairs will be

25   used, although others are contemplated. Longer polynucleotides encoding 250, 500, 1000, 1212, 1500, 2000, 2500, 3000 or 3431 bases and longer are contemplated as well. Such oligonucleotides will find use, for example, as probes in Southern and Northern blots and as primers in amplification reactions.

30   Suitable hybridization conditions will be well known to those of skill in the art. In certain applications, for example, substitution of amino acids by site-directed mutagenesis, it

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is appreciated that lower stringency conditions are required. Under these conditions, hybridization may occur even though the sequences of probe and target strand are not perfectly complementary, but are mismatched at one or more positions. Conditions may be rendered less stringent by increasing salt concentration and decreasing temperature. For example, a medium stringency condition could be provided by about 0.1 to 0.25 M NaCl at temperatures of about 37°C to about 55°C, while a low stringency condition could be provided by about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

In other embodiments, hybridization may be achieved under conditions of, for example, 50 mM Tris-HCl (pH 8.3), 75 mM KCl, 3 mM $MgCl_2$, 10 mM dithiothreitol, at temperatures between approximately 20°C to about 37°C. Other hybridization conditions utilized could include approximately 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 µM $MgCl_2$, at temperatures ranging from approximately 40°C to about 72°C. Formamide and SDS also may be used to alter the hybridization conditions.

One method of using probes and primers of the present invention is in the search for genes related to MCIP1, MCIP2, or MCIP3 or, more particularly, homologs of MCIP1, MCIP2 or MCIP3 from other species. Normally, the target DNA will be a genomic or cDNA library, although screening may involve analysis of RNA molecules. By varying the stringency of hybridization, and the region of the probe, different degrees of homology may be discovered.

Another way of exploiting probes and primers of the present invention is in site-directed, or site-specific mutagenesis. Site-specific mutagenesis is a technique useful in the preparation of individual peptides, or biologically functional equivalent proteins or peptides, through specific mutagenesis of the underlying DNA. The technique further provides a ready ability to prepare and test sequence variants, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use

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of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 17 to 25 nucleotides in length is preferred, with about 5 to 10 residues on both sides of the junction of the sequence being altered.

The technique typically employs a bacteriophage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage vectors are commercially available and their use is generally well known to those skilled in the art. Double stranded plasmids are also routinely employed in site directed mutagenesis, which eliminates the step of transferring the gene of interest from a phage to a plasmid.

In general, site-directed mutagenesis is performed by first obtaining a single-stranded vector, or melting of two strands of a double-stranded vector which includes within its sequence a DNA sequence encoding the desired protein. An oligonucleotide primer bearing the desired mutated sequence is synthetically prepared. This primer is then annealed with the single-stranded DNA preparation, taking into account the degree of mismatch when selecting hybridization conditions, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected that include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected gene using site-directed mutagenesis is provided as a means of producing potentially useful species and is not meant to be limiting, as there are other ways in which sequence variants of genes may be
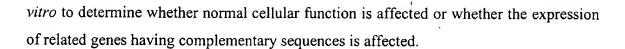
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obtained. For example, recombinant vectors encoding the desired gene may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants.

C. Antisense Constructs

5   Antisense methodology takes advantage of the fact that nucleic acids tend to pair with "complementary" sequences. By complementary, it is meant that polynucleotides are those which are capable of base-pairing according to the standard Watson-Crick complementarity rules. That is, the larger purines will base pair with the smaller pyrimidines to form combinations of guanine paired with cytosine (G:C) and adenine

10   paired with either thymine (A:T) in the case of DNA, or adenine paired with uracil (A:U) in the case of RNA. Inclusion of less common bases such as inosine, 5-methylcytosine, 6-methyladenine, hypoxanthine and others in hybridizing sequences does not interfere with pairing.

15   Targeting double-stranded (ds) DNA with polynucleotides leads to triple-helix formation; targeting RNA will lead to double-helix formation. Antisense polynucleotides, when introduced into a target cell, specifically bind to their target polynucleotide and interfere with transcription, RNA processing, transport, translation and/or stability. Antisense RNA constructs, or DNA encoding such antisense RNA's,

20   may be employed to inhibit gene transcription or translation or both within a host cell, either *in vitro* or *in vivo*, such as within a host animal, including a human subject.

       Antisense constructs may be designed to bind to the promoter and other control regions, exons, introns or even exon-intron boundaries of a gene. It is contemplated that

25   the most effective antisense constructs will include regions complementary to intron/exon splice junctions. Thus, it is proposed that a preferred embodiment includes an antisense construct with complementarity to regions within 50-200 bases of an intron-exon splice junction. It has been observed that some exon sequences can be included in the construct without seriously affecting the target selectivity thereof. The amount of exonic material

30   included will vary depending on the particular exon and intron sequences used. One can readily test whether too much exon DNA is included simply by testing the constructs *in*

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vitro to determine whether normal cellular function is affected or whether the expression of related genes having complementary sequences is affected.

As stated above, "complementary" or "antisense" means polynucleotide sequences that are substantially complementary over their entire length and have very few base mismatches. For example, sequences of fifteen bases in length may be termed complementary when they have complementary nucleotides at thirteen or fourteen positions. Naturally, sequences which are completely complementary will be sequences which are entirely complementary throughout their entire length and have no base mismatches. Other sequences with lower degrees of homology also are contemplated. For example, an antisense construct which has limited regions of high homology, but also contains a non-homologous region (*e.g.*, ribozyme; see below) could be designed. These molecules, though having less than 50% homology, would bind to target sequences under appropriate conditions.

It may be advantageous to combine portions of genomic DNA with cDNA or synthetic sequences to generate specific constructs. For example, where an intron is desired in the ultimate construct, a genomic clone will need to be used. The cDNA or a synthesized polynucleotide may provide more convenient restriction sites for the remaining portion of the construct and, therefore, would be used for the rest of the sequence.

D.   Ribozymes

Although proteins traditionally have been used for catalysis of nucleic acids, another class of macromolecules has emerged as useful in this endeavor. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cook, 1987; Gerlach *et al.*, 1987; Forster and Symons, 1987). For example, a large number of ribozymes accelerate phosphoester transfer reactions with a high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cook *et al.*, 1981; Michel and Westhof, 1990; Reinhold-Hurek and Shub, 1992). This

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specificity has been attributed to the requirement that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

5   Ribozyme catalysis has primarily been observed as part of sequence-specific cleavage/ligation reactions involving nucleic acids (Joyce, 1989; Cook *et al.*, 1981). For example, U.S. Patent 5,354,855 reports that certain ribozymes can act as endonucleases with a sequence specificity greater than that of known ribonucleases and approaching that of the DNA restriction enzymes. Thus, sequence-specific ribozyme-mediated inhibition

10   of gene expression may be particularly suited to therapeutic applications (Scanlon *et al.*, 1991; Sarver *et al.*, 1990). Recently, it was reported that ribozymes elicited genetic changes in some cells lines to which they were applied; the altered genes included the oncogenes H-ras, c-fos and genes of HIV. Most of this work involved the modification of a target mRNA, based on a specific mutant codon that is cleaved by a specific

15   ribozyme.

E.   Vectors for Cloning, Gene Transfer and Expression

          Within certain embodiments expression vectors are employed to express a MCIP polypeptide product, which can then be purified and, for example, be used to vaccinate

20   animals to generate antisera or monoclonal antibody with which further studies may be conducted. In other embodiments, the expression vectors are used in gene therapy. Expression requires that appropriate signals be provided in the vectors, and which include various regulatory elements, such as enhancers/promoters from both viral and mammalian sources that drive expression of the genes of interest in host cells. Elements

25   designed to optimize messenger RNA stability and translatability in host cells also are defined. The conditions for the use of a number of dominant drug selection markers for establishing permanent, stable cell clones expressing the products are also provided, as is an element that links expression of the drug selection markers to expression of the polypeptide.

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(i)   Regulatory Elements

Throughout this application, the term "expression construct" is meant to include any type of genetic construct containing a nucleic acid coding for a gene product in which part or all of the nucleic acid encoding sequence is capable of being transcribed. The transcript may be translated into a protein, but it need not be.   In certain embodiments, expression includes both transcription of a gene and translation of mRNA into a gene product. In other embodiments, expression only includes transcription of the nucleic acid encoding a gene of interest.

In certain embodiments, the nucleic acid encoding a gene product is under transcriptional control of a promoter. A "promoter" refers to a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate the specific transcription of a gene. The phrase "under transcriptional control" means that the promoter is in the correct location and orientation in relation to the nucleic acid to control RNA polymerase initiation and expression of the gene.

The term promoter will be used here to refer to a group of transcriptional control modules that are clustered around the initiation site for RNA polymerase II. Much of the thinking about how promoters are organized derives from analyses of several viral promoters, including those for the HSV thymidine kinase (*tk*) and SV40 early transcription units.   These studies, augmented by more recent work, have shown that promoters are composed of discrete functional modules, each consisting of approximately 7-20 bp of DNA, and containing one or more recognition sites for transcriptional activator or repressor proteins.

At least one module in each promoter functions to position the start site for RNA synthesis. The best known example of this is the TATA box, but in some promoters lacking a TATA box, such as the promoter for the mammalian terminal deoxynucleotidyl transferase gene and the promoter for the SV40 late genes, a discrete element overlying the start site itself helps to fix the place of initiation.

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Additional promoter elements regulate the frequency of transcriptional initiation. Typically, these are located in the region 30-110 bp upstream of the start site, although a number of promoters have recently been shown to contain functional elements downstream of the start site as well. The spacing between promoter elements frequently

5   is flexible, so that promoter function is preserved when elements are inverted or moved relative to one another. In the tk promoter, the spacing between promoter elements can be increased to 50 bp apart before activity begins to decline. Depending on the promoter, it appears that individual elements can function either co-operatively or independently to activate transcription.

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In certain embodiments, the native MCIP promoter will be employed to drive expression of either the corresponding MCIP gene, a heterologous MCIP gene, a screenable or selectable marker gene, or any other gene of interest. Of particular interest is the 700 bp immediately upstream of Exon 4 of the human MCIP gene. As discussed

15   above, this region contains a high concentration of binding sites for the transcription factor NFAT and therefore is likely to play an important regulatory function, especially in light of the existence of a transcript initiating at Exon 4.

In other embodiments, the human cytomegalovirus (CMV) immediate early gene

20   promoter, the SV40 early promoter, the Rous sarcoma virus long terminal repeat, rat insulin promoter and glyceraldehyde-3-phosphate dehydrogenase can be used to obtain high-level expression of the coding sequence of interest. The use of other viral or mammalian cellular or bacterial phage promoters which are well-known in the art to achieve expression of a coding sequence of interest is contemplated as well, provided that

25   the levels of expression are sufficient for a given purpose.

By employing a promoter with well-known properties, the level and pattern of expression of the protein of interest following transfection or transformation can be optimized. Further, selection of a promoter that is regulated in response to specific

30   physiologic signals can permit inducible expression of the gene product. Tables 2 and 3 list several regulatory elements that may be employed, in the context of the present

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invention, to regulate the expression of the gene of interest. This list is not intended to be exhaustive of all the possible elements involved in the promotion of gene expression but, merely, to be exemplary thereof.

5   Enhancers are genetic elements that increase transcription from a promoter located at a distant position on the same molecule of DNA. Enhancers are organized much like promoters. That is, they are composed of many individual elements, each of which binds to one or more transcriptional proteins.

10   The basic distinction between enhancers and promoters is operational. An enhancer region as a whole must be able to stimulate transcription at a distance; this need not be true of a promoter region or its component elements. On the other hand, a promoter must have one or more elements that direct initiation of RNA synthesis at a particular site and in a particular orientation, whereas enhancers lack these specificities.
15   Promoters and enhancers are often overlapping and contiguous, often seeming to have a very similar modular organization.

       Below is a list of viral promoters, cellular promoters/enhancers and inducible promoters/enhancers that could be used in combination with the nucleic acid encoding a
20   gene of interest in an expression construct (Table 2 and Table 3). Additionally, any promoter/enhancer combination (as per the Eukaryotic Promoter Data Base EPDB) could also be used to drive expression of the gene. Eukaryotic cells can support cytoplasmic transcription from certain bacterial promoters if the appropriate bacterial polymerase is provided, either as part of the delivery complex or as an additional genetic expression
25   construct.

TABLE 2

Promoter and/or Enhancer

Promoter/Enhancer	References
Immunoglobulin Heavy Chain	Banerji *et al.*, 1983; Gilles *et al.*, 1983; Grosschedl *et al.*, 1985; Atchinson *et al.*, 1986, 1987; Imler *et al.*, 1987; Weinberger *et al.*, 1984; Kiledjian *et al.*, 1988; Porton *et al.*; 1990
Immunoglobulin Light Chain	Queen *et al.*, 1983; Picard *et al.*, 1984
T-Cell Receptor	Luria *et al.*, 1987; Winoto *et al.*, 1989; Redondo *et al.*; 1990
HLA DQ a and/or DQ β	Sullivan *et al.*, 1987
β-Interferon	Goodbourn *et al.*, 1986; Fujita *et al.*, 1987; Goodbourn *et al.*, 1988
Interleukin-2	Greene *et al.*, 1989
Interleukin-2 Receptor	Greene *et al.*, 1989; Lin *et al.*, 1990
MHC Class II 5	Koch *et al.*, 1989
MHC Class II HLA-DRa	Sherman *et al.*, 1989
β-Actin	Kawamoto *et al.*, 1988; Ng *et al.*; 1989
Muscle Creatine Kinase (MCK)	Jaynes *et al.*, 1988; Horlick *et al.*, 1989; Johnson *et al.*, 1989
Prealbumin (Transthyretin)	Costa *et al.*, 1988
Elastase I	Ornitz *et al.*, 1987
Metallothionein (MTII)	Karin *et al.*, 1987; Culotta *et al.*, 1989
Collagenase	Pinkert *et al.*, 1987; Angel *et al.*, 1987a
Albumin	Pinkert *et al.*, 1987; Tronche *et al.*, 1989, 1990
α-Fetoprotein	Godbout *et al.*, 1988; Campere *et al.*, 1989
t-Globin	Bodine *et al.*, 1987; Perez-Stable *et al.*, 1990
β-Globin	Trudel *et al.*, 1987
c-fos	Cohen *et al.*, 1987
c-HA-*ras*	Triesman, 1986; Deschamps *et al.*, 1985
Insulin	Edlund *et al.*, 1985
Neural Cell Adhesion Molecule (NCAM)	Hirsh *et al.*, 1990

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TABLE 2	
Promoter and/or Enhancer	
Promoter/Enhancer	References
α_1-Antitrypain	Latimer et al., 1990
H2B (TH2B) Histone	Hwang et al., 1990
Mouse and/or Type I Collagen	Ripe et al., 1989
Glucose-Regulated Proteins (GRP94 and GRP78)	Chang et al., 1989
Rat Growth Hormone	Larsen et al., 1986
Human Serum Amyloid A (SAA)	Edbrooke et al., 1989
Troponin I (TN I)	Yutzey et al., 1989
Platelet-Derived Growth Factor (PDGF)	Pech et al., 1989
Duchenne Muscular Dystrophy	Klamut et al., 1990
SV40	Banerji et al., 1981; Moreau et al., 1981; Sleigh et al., 1985; Firak et al., 1986; Herr et al., 1986; Imbra et al., 1986; Kadesch et al., 1986; Wang et al., 1986; Ondek et al., 1987; Kuhl et al., 1987; Schaffner et al., 1988
Polyoma	Swartzendruber et al., 1975; Vasseur et al., 1980; Katinka et al., 1980, 1981; Tyndell et al., 1981; Dandolo et al., 1983; de Villiers et al., 1984; Hen et al., 1986; Satake et al., 1988; Campbell and/or Villarreal, 1988
Retroviruses	Kriegler et al., 1982, 1983; Levinson et al., 1982; Kriegler et al., 1983, 1984a, b, 1988; Bosze et al., 1986; Miksicek et al., 1986; Celander et al., 1987; Thiesen et al., 1988; Celander et al., 1988; Choi et al., 1988; Reisman et al., 1989
Papilloma Virus	Campo et al., 1983; Lusky et al., 1983; Spandidos and/or Wilkie, 1983; Spalholz et al., 1985; Lusky et al., 1986; Cripe et al., 1987; Gloss et al., 1987; Hirochika et al., 1987; Stephens et al., 1987
Hepatitis B Virus	Bulla et al., 1986; Jameel et al., 1986; Shaul et al., 1987; Spandau et al., 1988; Vannice et al., 1988
Human Immunodeficiency Virus	Muesing et al., 1987; Hauber et al., 1988; Jakobovits et al., 1988; Feng et al., 1988; Takebe et al., 1988; Rosen et al., 1988; Berkhout et al., 1989; Laspia et al., 1989; Sharp et al., 1989; Braddock et al., 1989

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TABLE 2

Promoter and/or Enhancer

Promoter/Enhancer	References
Cytomegalovirus (CMV)	Weber *et al.*, 1984; Boshart *et al.*, 1985; Foecking *et al.*, 1986
Gibbon Ape Leukemia Virus	Holbrook *et al.*, 1987; Quinn *et al.*, 1989

TABLE 3

Inducible Elements

Element	Inducer	References
MT II	Phorbol Ester (TFA) Heavy metals	Palmiter *et al.*, 1982; Haslinger *et al.*, 1985; Searle *et al.*, 1985; Stuart *et al.*, 1985; Imagawa *et al.*, 1987, Karin *et al.*, 1987; Angel *et al.*, 1987b; McNeall *et al.*, 1989
MMTV (mouse mammary tumor virus)	Glucocorticoids	Huang *et al.*, 1981; Lee *et al.*, 1981; Majors *et al.*, 1983; Chandler *et al.*, 1983; Ponta *et al.*, 1985; Sakai *et al.*, 1988
β-Interferon	poly(rI)x poly(rc)	Tavernier *et al.*, 1983
Adenovirus 5 E2	EIA	Imperiale *et al.*, 1984
Collagenase	Phorbol Ester (TPA)	Angel *et al.*, 1987a
Stromelysin	Phorbol Ester (TPA)	Angel *et al.*, 1987b
SV40	Phorbol Ester (TPA)	Angel *et al.*, 1987b
Murine MX Gene	Interferon, Newcastle Disease Virus	Hug *et al.*, 1988
GRP78 Gene	A23187	Resendez *et al.*, 1988
α-2-Macroglobulin	IL-6	Kunz *et al.*, 1989
Vimentin	Serum	Rittling *et al.*, 1989
MHC Class I Gene H-2κb	Interferon	Blanar *et al.*, 1989
HSP70	EIA, SV40 Large T	Taylor *et al.*, 1989, 1990a, 1990b

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TABLE 3		
Inducible Elements		
Element	Inducer	References
	Antigen	
Proliferin	Phorbol Ester-TPA	Mordacq *et al.*, 1989
Tumor Necrosis Factor	PMA	Hensel *et al.*, 1989
Thyroid Stimulating Hormone α Gene	Thyroid Hormone	Chatterjee *et al.*, 1989

Of particular interest are muscle specific promoters, and more particularly, cardiac specific promoters. These include the myosin light chain-2 promoter (Franz *et al.*, 1994; Kelly *et al.*, 1995), the alpha actin promoter (Moss *et al.*, 1996), the troponin 1 promoter (Bhavsar *et al.*, 1996); the Na^+/Ca^{2+} exchanger promoter (Barnes *et al.*, 1997), the dystrophin promoter (Kimura *et al.*, 1997), the creatine kinase promoter (Ritchie, M.E., 1996), the alpha7 integrin promoter (Ziober & Kramer, 1996), the brain natriuretic peptide promoter (LaPointe *et al.*, 1996) and the alpha B-crystallin/small heat shock protein promoter (Gopal-Srivastava, R., 1995), alpha myosin heavy chain promoter (Yamauchi-Takihara *et al.*, 1989) and the ANF promoter (LaPointe *et al.*, 1988).

Where a cDNA insert is employed, one will typically desire to include a polyadenylation signal to effect proper polyadenylation of the gene transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention, and any such sequence may be employed such as human growth hormone and SV40 polyadenylation signals. Also contemplated as an element of the expression cassette is a terminator. These elements can serve to enhance message levels and to minimize read through from the cassette into other sequences.

(ii)   Selectable Markers

In certain embodiments of the invention, the cells contain nucleic acid constructs of the present invention, a cell may be identified *in vitro* or *in vivo* by including a marker in the expression construct. Such markers would confer an identifiable change to the cell

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permitting easy identification of cells containing the expression construct. Usually the inclusion of a drug selection marker aids in cloning and in the selection of transformants, for example, genes that confer resistance to neomycin, puromycin, hygromycin, DHFR, GPT, zeocin and histidinol are useful selectable markers. Alternatively, enzymes such as

5 herpes simplex virus thymidine kinase (*tk*) or chloramphenicol acetyltransferase (CAT) may be employed. Immunologic markers also can be employed. The selectable marker employed is not believed to be important, so long as it is capable of being expressed simultaneously with the nucleic acid encoding a gene product. Further examples of selectable markers are well known to one of skill in the art.

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(iii)   Multigene Constructs and IRES

In certain embodiments of the invention, the use of internal ribosome binding sites (IRES) elements are used to create multigene, or polycistronic, messages. IRES elements are able to bypass the ribosome scanning model of 5' methylated Cap dependent

15 translation and begin translation at internal sites (Pelletier and Sonenberg, 1988). IRES elements from two members of the picanovirus family (polio and encephalomyocarditis) have been described (Pelletier and Sonenberg, 1988), as well an IRES from a mammalian message (Macejak and Sarnow, 1991). IRES elements can be linked to heterologous open reading frames. Multiple open reading frames can be transcribed together, each

20 separated by an IRES, creating polycistronic messages. By virtue of the IRES element, each open reading frame is accessible to ribosomes for efficient translation. Multiple genes can be efficiently expressed using a single promoter/enhancer to transcribe a single message.

25 Any heterologous open reading frame can be linked to IRES elements. This includes genes for secreted proteins, multi-subunit proteins, encoded by independent genes, intracellular or membrane-bound proteins and selectable markers. In this way, expression of several proteins can be simultaneously engineered into a cell with a single construct and a single selectable marker.

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(iv)   Delivery of Expression Vectors

There are a number of ways in which expression vectors may introduced into cells. In certain embodiments of the invention, the expression construct comprises a virus or engineered construct derived from a viral genome. The ability of certain viruses to enter cells via receptor-mediated endocytosis, to integrate into host cell genome and express viral genes stably and efficiently have made them attractive candidates for the transfer of foreign genes into mammalian cells (Ridgeway, 1988; Nicolas and Rubenstein, 1988; Baichwal and Sugden, 1986; Temin, 1986). The first viruses used as gene vectors were DNA viruses including the papovaviruses (simian virus 40, bovine papilloma virus, and polyoma) (Ridgeway, 1988; Baichwal and Sugden, 1986) and adenoviruses (Ridgeway, 1988; Baichwal and Sugden, 1986). These have a relatively low capacity for foreign DNA sequences and have a restricted host spectrum. Furthermore, their oncogenic potential and cytopathic effects in permissive cells raise safety concerns. They can accommodate only up to 8 kB of foreign genetic material but can be readily introduced in a variety of cell lines and laboratory animals (Nicolas and Rubenstein, 1988; Temin, 1986).

One of the preferred methods for *in vivo* delivery involves the use of an adenovirus expression vector. "Adenovirus expression vector" is meant to include those constructs containing adenovirus sequences sufficient to (a) support packaging of the construct and (b) to express an antisense polynucleotide that has been cloned therein. In this context, expression does not require that the gene product be synthesized.

The expression vector comprises a genetically engineered form of adenovirus. Knowledge of the genetic organization of adenovirus, a 36 kB, linear, double-stranded DNA virus, allows substitution of large pieces of adenoviral DNA with foreign sequences up to 7 kB (Grunhaus and Horwitz, 1992). In contrast to retrovirus, the adenoviral infection of host cells does not result in chromosomal integration because adenoviral DNA can replicate in an episomal manner without potential genotoxicity. Also, adenoviruses are structurally stable, and no genome rearrangement has been detected after extensive amplification. Adenovirus can infect virtually all epithelial cells

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regardless of their cell cycle stage. So far, adenoviral infection appears to be linked only to mild disease such as acute respiratory disease in humans.

Adenovirus is particularly suitable for use as a gene transfer vector because of its mid-sized genome, ease of manipulation, high titer, wide target cell range and high infectivity. Both ends of the viral genome contain 100-200 base pair inverted repeats (ITRs), which are *cis* elements necessary for viral DNA replication and packaging. The early (E) and late (L) regions of the genome contain different transcription units that are divided by the onset of viral DNA replication. The E1 region (E1A and E1B) encodes proteins responsible for the regulation of transcription of the viral genome and a few cellular genes. The expression of the E2 region (E2A and E2B) results in the synthesis of the proteins for viral DNA replication. These proteins are involved in DNA replication, late gene expression and host cell shut-off (Renan, 1990). The products of the late genes, including the majority of the viral capsid proteins, are expressed only after significant processing of a single primary transcript issued by the major late promoter (MLP). The MLP, (located at 16.8 m.u.) is particularly efficient during the late phase of infection, and all the mRNA's issued from this promoter possess a 5'-tripartite leader (TPL) sequence which makes them preferred mRNA's for translation.

In a current system, recombinant adenovirus is generated from homologous recombination between shuttle vector and provirus vector. Due to the possible recombination between two proviral vectors, wild-type adenovirus may be generated from this process. Therefore, it is critical to isolate a single clone of virus from an individual plaque and examine its genomic structure.

Generation and propagation of the current adenovirus vectors, which are replication deficient, depend on a unique helper cell line, designated 293, which was transformed from human embryonic kidney cells by Ad5 DNA fragments and constitutively expresses E1 proteins (Graham *et al.*, 1977). Since the E3 region is dispensable from the adenovirus genome (Jones and Shenk, 1978), the current adenovirus vectors, with the help of 293 cells, carry foreign DNA in either the E1, the D3 or both

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regions (Graham and Prevec, 1991). In nature, adenovirus can package approximately 105% of the wild-type genome (Ghosh-Choudhury *et al.*, 1987), providing capacity for about 2 extra kb of DNA. Combined with the approximately 5.5 kb of DNA that is replaceable in the E1 and E3 regions, the maximum capacity of the current adenovirus vector is under 7.5 kb, or about 15% of the total length of the vector. More than 80% of the adenovirus viral genome remains in the vector backbone and is the source of vector-borne cytotoxicity. Also, the replication deficiency of the E1-deleted virus is incomplete. For example, leakage of viral gene expression has been observed with the currently available vectors at high multiplicities of infection (MOI) (Mulligan, 1993).
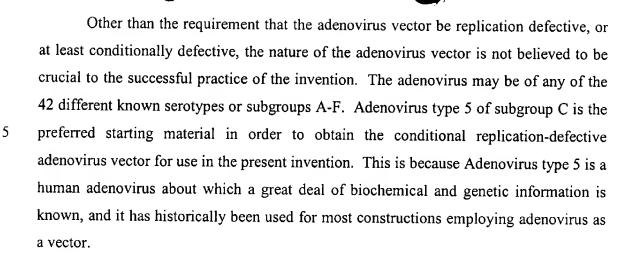
Helper cell lines may be derived from human cells such as human embryonic kidney cells, muscle cells, hematopoietic cells or other human embryonic mesenchymal or epithelial cells. Alternatively, the helper cells may be derived from the cells of other mammalian species that are permissive for human adenovirus. Such cells include, *e.g.*, Vero cells or other monkey embryonic mesenchymal or epithelial cells. As stated above, the preferred helper cell line is 293.

Racher *et al.* (1995) disclosed improved methods for culturing 293 cells and propagating adenovirus. In one format, natural cell aggregates are grown by inoculating individual cells into 1 liter siliconized spinner flasks (Techne, Cambridge, UK) containing 100-200 ml of medium. Following stirring at 40 rpm, the cell viability is estimated with trypan blue. In another format, Fibra-Cel microcarriers (Bibby Sterlin, Stone, UK) (5 g/l) is employed as follows. A cell inoculum, resuspended in 5 ml of medium, is added to the carrier (50 ml) in a 250 ml Erlenmeyer flask and left stationary, with occasional agitation, for 1 to 4 h. The medium is then replaced with 50 ml of fresh medium and shaking initiated. For virus production, cells are allowed to grow to about 80% confluence, after which time the medium is replaced (to 25% of the final volume) and adenovirus added at an MOI of 0.05. Cultures are left stationary overnight, following which the volume is increased to 100% and shaking commenced for another 72 h.

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Other than the requirement that the adenovirus vector be replication defective, or at least conditionally defective, the nature of the adenovirus vector is not believed to be crucial to the successful practice of the invention. The adenovirus may be of any of the 42 different known serotypes or subgroups A-F. Adenovirus type 5 of subgroup C is the preferred starting material in order to obtain the conditional replication-defective adenovirus vector for use in the present invention. This is because Adenovirus type 5 is a human adenovirus about which a great deal of biochemical and genetic information is known, and it has historically been used for most constructions employing adenovirus as a vector.

As stated above, the typical vector according to the present invention is replication defective and will not have an adenovirus E1 region. Thus, it will be most convenient to introduce the polynucleotide encoding the gene of interest at the position from which the E1-coding sequences have been removed. However, the position of insertion of the construct within the adenovirus sequences is not critical to the invention. The polynucleotide encoding the gene of interest may also be inserted in lieu of the deleted E3 region in E3 replacement vectors, as described by Karlsson *et al.* (1986), or in the E4 region where a helper cell line or helper virus complements the E4 defect.

Adenovirus is easy to grow and manipulate and exhibits broad host range *in vitro* and *in vivo*. This group of viruses can be obtained in high titers, *e.g.*, 10^9-10^{12} plaque-forming units per ml, and they are highly infective. The life cycle of adenovirus does not require integration into the host cell genome. The foreign genes delivered by adenovirus vectors are episomal and, therefore, have low genotoxicity to host cells. No side effects have been reported in studies of vaccination with wild-type adenovirus (Couch *et al.*, 1963; Top *et al.*, 1971), demonstrating their safety and therapeutic potential as *in vivo* gene transfer vectors.

Adenovirus vectors have been used in eukaryotic gene expression (Levrero *et al.*, 1991; Gomez-Foix *et al.*, 1992) and vaccine development (Grunhaus and Horwitz, 1992; Graham and Prevec, 1991). Recently, animal studies suggested that recombinant

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adenovirus could be used for gene therapy (Stratford-Perricaudet and Perricaudet, 1991; Stratford-Perricaudet *et al.*, 1990; Rich *et al.*, 1993). Studies in administering recombinant adenovirus to different tissues include trachea instillation (Rosenfeld *et al.*, 1991; Rosenfeld *et al.*, 1992), muscle injection (Ragot *et al.*, 1993), peripheral intravenous injections (Herz and Gerard, 1993) and stereotactic inoculation into the brain (Le Gal La Salle *et al.*, 1993).

The retroviruses are a group of single-stranded RNA viruses characterized by an ability to convert their RNA to double-stranded DNA in infected cells by a process of reverse-transcription (Coffin, 1990). The resulting DNA then stably integrates into cellular chromosomes as a provirus and directs synthesis of viral proteins. The integration results in the retention of the viral gene sequences in the recipient cell and its descendants. The retroviral genome contains three genes, gag, pol, and env that code for capsid proteins, polymerase enzyme, and envelope components, respectively. A sequence found upstream from the gag gene contains a signal for packaging of the genome into virions. Two long terminal repeat (LTR) sequences are present at the 5' and 3' ends of the viral genome. These contain strong promoter and enhancer sequences and are also required for integration in the host cell genome (Coffin, 1990).

In order to construct a retroviral vector, a nucleic acid encoding a gene of interest is inserted into the viral genome in the place of certain viral sequences to produce a virus that is replication-defective. In order to produce virions, a packaging cell line containing the gag, pol, and env genes but without the LTR and packaging components is constructed (Mann *et al.*, 1983). When a recombinant plasmid containing a cDNA, together with the retroviral LTR and packaging sequences is introduced into this cell line (by calcium phosphate precipitation for example), the packaging sequence allows the RNA transcript of the recombinant plasmid to be packaged into viral particles, which are then secreted into the culture media (Nicolas and Rubenstein, 1988; Temin, 1986; Mann *et al.*, 1983). The media containing the recombinant retroviruses is then collected, optionally concentrated, and used for gene transfer. Retroviral vectors are able to infect a
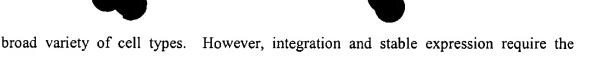
49

broad variety of cell types. However, integration and stable expression require the division of host cells (Paskind *et al.*, 1975).

A novel approach designed to allow specific targeting of retrovirus vectors was recently developed based on the chemical modification of a retrovirus by the chemical addition of lactose residues to the viral envelope. This modification could permit the specific infection of hepatocytes via sialoglycoprotein receptors.

A different approach to targeting of recombinant retroviruses was designed in which biotinylated antibodies against a retroviral envelope protein and against a specific cell receptor were used. The antibodies were coupled via the biotin components by using streptavidin (Roux *et al.*, 1989). Using antibodies against major histocompatibility complex class I and class II antigens, they demonstrated the infection of a variety of human cells that bore those surface antigens with an ecotropic virus *in vitro* (Roux *et al.*, 1989).

There are certain limitations to the use of retrovirus vectors in all aspects of the present invention. For example, retrovirus vectors usually integrate into random sites in the cell genome. This can lead to insertional mutagenesis through the interruption of host genes or through the insertion of viral regulatory sequences that can interfere with the function of flanking genes (Varmus *et al.*, 1981). Another concern with the use of defective retrovirus vectors is the potential appearance of wild-type replication-competent virus in the packaging cells. This can result from recombination events in which the intact- sequence from the recombinant virus inserts upstream from the gag, pol, env sequence integrated in the host cell genome. However, new packaging cell lines are now available that should greatly decrease the likelihood of recombination (Markowitz *et al.*, 1988; Hersdorffer *et al.*, 1990).

Other viral vectors may be employed as expression constructs in the present invention. Vectors derived from viruses such as vaccinia virus (Ridgeway, 1988; Baichwal and Sugden, 1986; Coupar *et al.*, 1988) adeno-associated virus (AAV)

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(Ridgeway, 1988; Baichwal and Sugden, 1986; Hermonat and Muzycska, 1984) and herpesviruses may be employed. They offer several attractive features for various mammalian cells (Friedmann, 1989; Ridgeway, 1988; Baichwal and Sugden, 1986; Coupar *et al.*, 1988; Horwich *et al.*, 1990).

With the recent recognition of defective hepatitis B viruses, new insight was gained into the structure-function relationship of different viral sequences. *In vitro* studies showed that the virus could retain the ability for helper-dependent packaging and reverse transcription despite the deletion of up to 80% of its genome (Horwich *et al.*, 1990). This suggested that large portions of the genome could be replaced with foreign genetic material. The hepatotropism and persistence (integration) were particularly attractive properties for liver-directed gene transfer. Chang *et al.*, recently introduced the chloramphenicol acetyltransferase (CAT) gene into duck hepatitis B virus genome in the place of the polymerase, surface, and pre-surface coding sequences. It was co-transfected with wild-type virus into an avian hepatoma cell line. Culture media containing high titers of the recombinant virus were used to infect primary duckling hepatocytes. Stable CAT gene expression was detected for at least 24 days after transfection (Chang *et al.*, 1991).

In order to effect expression of sense or antisense gene constructs, the expression construct must be delivered into a cell. This delivery may be accomplished *in vitro*, as in laboratory procedures for transforming cells lines, or *in vivo* or *ex vivo*, as in the treatment of certain disease states. One mechanism for delivery is via viral infection where the expression construct is encapsidated in an infectious viral particle.

Several non-viral methods for the transfer of expression constructs into cultured mammalian cells also are contemplated by the present invention. These include calcium phosphate precipitation (Graham and Van Der Eb, 1973; Chen and Okayama, 1987; Rippe *et al.*, 1990) DEAE-dextran (Gopal, 1985), electroporation (Tur-Kaspa *et al.*, 1986; Potter *et al.*, 1984), direct microinjection (Harland and Weintraub, 1985), DNA-loaded liposomes (Nicolau and Sene, 1982; Fraley *et al.*, 1979) and lipofectamine-DNA

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complexes, cell sonication (Fechheimer *et al.*, 1987), gene bombardment using high velocity microprojectiles (Yang *et al.*, 1990), and receptor-mediated transfection (Wu and Wu, 1987; Wu and Wu, 1988). Some of these techniques may be successfully adapted for *in vivo* or *ex vivo* use.

5

Once the expression construct has been delivered into the cell the nucleic acid encoding the gene of interest may be positioned and expressed at different sites. In certain embodiments, the nucleic acid encoding the gene may be stably integrated into the genome of the cell. This integration may be in the cognate location and orientation via

10   homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the nucleic acid may be stably maintained in the cell as a separate, episomal segment of DNA. Such nucleic acid segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. How the

15   expression construct is delivered to a cell and where in the cell the nucleic acid remains is dependent on the type of expression construct employed.

In yet another embodiment of the invention, the expression construct may simply consist of naked recombinant DNA or plasmids. Transfer of the construct may be

20   performed by any of the methods mentioned above which physically or chemically permeabilize the cell membrane. This is particularly applicable for transfer *in vitro* but it may be applied to *in vivo* use as well. Dubensky *et al.* (1984) successfully injected polyomavirus DNA in the form of calcium phosphate precipitates into liver and spleen of adult and newborn mice demonstrating active viral replication and acute infection.

25   Benvenisty and Neshif (1986) also demonstrated that direct intraperitoneal injection of calcium phosphate-precipitated plasmids results in expression of the transfected genes. It is envisioned that DNA encoding a gene of interest may also be transferred in a similar manner *in vivo* and express the gene product.

30   In still another embodiment of the invention for transferring a naked DNA expression construct into cells may involve particle bombardment. This method depends

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on the ability to accelerate DNA-coated microprojectiles to a high velocity allowing them to pierce cell membranes and enter cells without killing them (Klein *et al.*, 1987). Several devices for accelerating small particles have been developed. One such device relies on a high voltage discharge to generate an electrical current, which in turn provides

5   the motive force (Yang *et al.*, 1990). The microprojectiles used have consisted of biologically inert substances such as tungsten or gold beads.

Selected organs including the liver, skin, and muscle tissue of rats and mice have been bombarded *in vivo* (Yang *et al.*, 1990; Zelenin *et al.*, 1991). This may require

10 surgical exposure of the tissue or cells, to eliminate any intervening tissue between the gun and the target organ, *i.e., ex vivo* treatment. Again, DNA encoding a particular gene may be delivered via this method and still be incorporated by the present invention.

In a further embodiment of the invention, the expression construct may be

15 entrapped in a liposome. Liposomes are vesicular structures characterized by a phospholipid bilayer membrane and an inner aqueous medium. Multilamellar liposomes have multiple lipid layers separated by aqueous medium. They form spontaneously when phospholipids are suspended in an excess of aqueous solution. The lipid components undergo self-rearrangement before the formation of closed structures and entrap water

20 and dissolved solutes between the lipid bilayers (Ghosh and Bachhawat, 1991). Also contemplated are lipofectamine-DNA complexes.

Liposome-mediated nucleic acid delivery and expression of foreign DNA *in vitro* has been very successful. Wong *et al.*, (1980) demonstrated the feasibility of liposome-

25 mediated delivery and expression of foreign DNA in cultured chick embryo, HeLa and hepatoma cells. Nicolau *et al.*, (1987) accomplished successful liposome-mediated gene transfer in rats after intravenous injection.

In certain embodiments of the invention, the liposome may be complexed with a

30 hemagglutinating virus (HVJ). This has been shown to facilitate fusion with the cell membrane and promote cell entry of liposome-encapsulated DNA (Kaneda *et al.*, 1989).

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In other embodiments, the liposome may be complexed or employed in conjunction with nuclear non-histone chromosomal proteins (HMG-1) (Kato *et al.*, 1991). In yet further embodiments, the liposome may be complexed or employed in conjunction with both HVJ and HMG-1. In that such expression constructs have been successfully employed in transfer and expression of nucleic acid *in vitro* and *in vivo*, then they are applicable for the present invention. Where a bacterial promoter is employed in the DNA construct, it also will be desirable to include within the liposome an appropriate bacterial polymerase.

Other expression constructs which can be employed to deliver a nucleic acid encoding a particular gene into cells are receptor-mediated delivery vehicles. These take advantage of the selective uptake of macromolecules by receptor-mediated endocytosis in almost all eukaryotic cells. Because of the cell type-specific distribution of various receptors, the delivery can be highly specific (Wu and Wu, 1993).

Receptor-mediated gene targeting vehicles generally consist of two components: a cell receptor-specific ligand and a DNA-binding agent. Several ligands have been used for receptor-mediated gene transfer. The most extensively characterized ligands are asialoorosomucoid (ASOR) (Wu and Wu, 1987) and transferrin (Wagner *et al.*, 1990). Recently, a synthetic neoglycoprotein, which recognizes the same receptor as ASOR, has been used as a gene delivery vehicle (Ferkol *et al.*, 1993; Perales *et al.*, 1994) and epidermal growth factor (EGF) has also been used to deliver genes to squamous carcinoma cells (Myers, EPO 0273085).

In other embodiments, the delivery vehicle may comprise a ligand and a liposome. For example, Nicolau *et al.*, (1987) employed lactosyl-ceramide, a galactose-terminal asialganglioside, incorporated into liposomes and observed an increase in the uptake of the insulin gene by hepatocytes. Thus, it is feasible that a nucleic acid encoding a particular gene also may be specifically delivered into a cell type by any number of receptor-ligand systems with or without liposomes. For example, epidermal growth factor (EGF) may be used as the receptor for mediated delivery of a nucleic acid into cells that exhibit upregulation of EGF receptor. Mannose can be used to target the

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mannose receptor on liver cells. Also, antibodies to CD5 (CLL), CD22 (lymphoma), CD25 (T-cell leukemia) and MAA (melanoma) can similarly be used as targeting moieties.

5   In certain embodiments, gene transfer may more easily be performed under *ex vivo* conditions. *Ex vivo* gene therapy refers to the isolation of cells from an animal, the delivery of a nucleic acid into the cells *in vitro*, and then the return of the modified cells back into an animal. This may involve the surgical removal of tissue/organs from an animal or the primary culture of cells and tissues.

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III.   Generating Antibodies Reactive With MCIP1, MCIP2 and MCIP3

          In another aspect, the present invention contemplates an antibody that is immunoreactive with a MCIP molecule of the present invention, or any portion thereof. An antibody can be a polyclonal or a monoclonal antibody. In a preferred embodiment,
15   an antibody is a monoclonal antibody. Means for preparing and characterizing antibodies are well known in the art (see, *e.g.,* Harlow and Lane, 1988).

          Briefly, a polyclonal antibody is prepared by immunizing an animal with an immunogen comprising a polypeptide of the present invention and collecting antisera
20   from that immunized animal. A wide range of animal species can be used for the production of antisera. Typically an animal used for production of anti-antisera is a non-human animal including rabbits, mice, rats, hamsters, pigs or horses. Because of the relatively large blood volume of rabbits, a rabbit is a preferred choice for production of polyclonal antibodies.

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          Antibodies, both polyclonal and monoclonal, specific for isoforms of antigen may be prepared using conventional immunization techniques, as will be generally known to those of skill in the art. A composition containing antigenic epitopes of the compounds of the present invention can be used to immunize one or more experimental animals, such
30   as a rabbit or mouse, which will then proceed to produce specific antibodies against the compounds of the present invention. Polyclonal antisera may be obtained, after allowing

time for antibody generation, simply by bleeding the animal and preparing serum samples from the whole blood.

It is proposed that the monoclonal antibodies of the present invention will find useful application in standard immunochemical procedures, such as ELISA and Western blot methods and in immunohistochemical procedures such as tissue staining, as well as in other procedures which may utilize antibodies specific to MCIP-related antigen epitopes. Additionally, it is proposed that monoclonal antibodies specific to the particular MCIP of different species may be utilized in other useful applications

In general, both polyclonal and monoclonal antibodies against MCIPs may be used in a variety of embodiments. For example, they may be employed in antibody cloning protocols to obtain cDNAs or genes encoding other MCIPs. They may also be used in inhibition studies to analyze the effects of MCIPs related peptides in cells or animals. MCIPs antibodies will also be useful in immunolocalization studies to analyze the distribution of MCIPs during various cellular events, for example, to determine the cellular or tissue-specific distribution of MCIPs polypeptides under different points in the cell cycle. A particularly useful application of such antibodies is in purifying native or recombinant MCIPs, for example, using an antibody affinity column. The operation of all such immunological techniques will be known to those of skill in the art in light of the present disclosure.

Means for preparing and characterizing antibodies are well known in the art (see, e.g., Harlow and Lane, 1988; incorporated herein by reference). More specific examples of monoclonal antibody preparation are given in the examples below.

As is well known in the art, a given composition may vary in its immunogenicity. It is often necessary therefore to boost the host immune system, as may be achieved by coupling a peptide or polypeptide immunogen to a carrier. Exemplary and preferred carriers are keyhole limpet hemocyanin (KLH) and bovine serum albumin (BSA). Other albumins such as ovalbumin, mouse serum albumin or rabbit serum albumin can also be
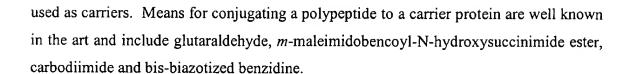
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used as carriers. Means for conjugating a polypeptide to a carrier protein are well known in the art and include glutaraldehyde, *m*-maleimidobencoyl-N-hydroxysuccinimide ester, carbodiimide and bis-biazotized benzidine.

5   As also is well known in the art, the immunogenicity of a particular immunogen composition can be enhanced by the use of non-specific stimulators of the immune response, known as adjuvants. Exemplary and preferred adjuvants include complete Freund's adjuvant (a non-specific stimulator of the immune response containing killed *Mycobacterium tuberculosis)*, incomplete Freund's adjuvants and aluminum hydroxide
10   adjuvant.

The amount of immunogen composition used in the production of polyclonal antibodies varies upon the nature of the immunogen as well as the animal used for immunization. A variety of routes can be used to administer the immunogen
15   (subcutaneous, intramuscular, intradermal, intravenous and intraperitoneal). The production of polyclonal antibodies may be monitored by sampling blood of the immunized animal at various points following immunization. A second, booster, injection may also be given. The process of boosting and titering is repeated until a suitable titer is achieved. When a desired level of immunogenicity is obtained, the
20   immunized animal can be bled and the serum isolated and stored, and/or the animal can be used to generate mAbs.

MAbs may be readily prepared through use of well-known techniques, such as those exemplified in U.S. Patent 4,196,265, incorporated herein by reference. Typically,
25   this technique involves immunizing a suitable animal with a selected immunogen composition, *e.g.*, a purified or partially purified MCIP protein, polypeptide or peptide or cell expressing high levels of MCIP. The immunizing composition is administered in a manner effective to stimulate antibody producing cells. Rodents such as mice and rats are preferred animals, however, the use of rabbit, sheep frog cells is also possible. The
30   use of rats may provide certain advantages (Goding, 1986), but mice are preferred, with

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the BALB/c mouse being most preferred as this is most routinely used and generally gives a higher percentage of stable fusions.

IV.   Diagnosing and Treating Defects in MCIPs

5   The inventors have shown MCIPs play an important role in the regulation of calcineurin, which in turn is a key regulator of cardiac hypetrophy. In addition, reduction in MCIP activity, which in turn can deregulate calcineurin and play in important role in cardiac disease.   Thus, in another embodiment, there are provided methods for diagnosing defects in MCIP expression and function. More specifically, point mutations,

10   deletions, insertions or regulatory pertubations relating to MCIPs may be assessed using standard technologies, as described below.

A.   Genetic Diagnosis

One embodiment of the instant invention comprises a method for detecting

15   variation in the expression of MCIP1, MCIP2 and MCIP3.   This may comprises determining that level of MCIP1, MCIP2 or MCIP3 or determining specific alterations in the expressed product.

A suitable biological sample can be any tissue or fluid. Various embodiments

20   include cells of the skin, muscle, facia, brain, prostate, breast, endometrium, lung, head & neck, pancreas, small intestine, blood cells, liver, testes, ovaries, colon, skin, stomach, esophagus, spleen, lymph node, bone marrow or kidney. Other embodiments include fluid samples such as peripheral blood, lymph fluid, ascites, serous fluid, pleural effusion, sputum, cerebrospinal fluid, lacrimal fluid, stool or urine.
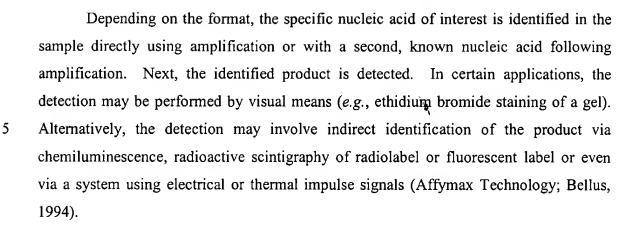
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Nucleic acid used is isolated from cells contained in the biological sample, according to standard methodologies (Sambrook *et al.*, 1989). The nucleic acid may be genomic DNA or fractionated or whole cell RNA. Where RNA is used, it may be desired to convert the RNA to a complementary DNA. In one embodiment, the RNA is whole

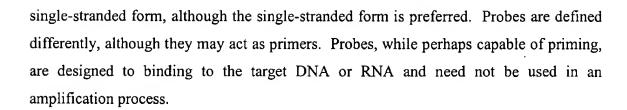30   cell RNA; in another, it is poly-A RNA. Normally, the nucleic acid is amplified.

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Depending on the format, the specific nucleic acid of interest is identified in the sample directly using amplification or with a second, known nucleic acid following amplification. Next, the identified product is detected. In certain applications, the detection may be performed by visual means (*e.g.*, ethidium bromide staining of a gel).

5   Alternatively, the detection may involve indirect identification of the product via chemiluminescence, radioactive scintigraphy of radiolabel or fluorescent label or even via a system using electrical or thermal impulse signals (Affymax Technology; Bellus, 1994).

10   Various types of defects may be identified by the present methods. Thus, "alterations" should be read as including deletions, insertions, point mutations and duplications. Point mutations result in stop codons, frameshift mutations or amino acid substitutions. Somatic mutations are those occurring in non-germline tissues. Germ-line tissue can occur in any tissue and are inherited. Mutations in and outside the coding

15   region also may affect the amount of MCIP produced, both by altering the transcription of the gene or in destabilizing or otherwise altering the processing of either the transcript (mRNA) or protein.

It is contemplated that other mutations in the MCIP genes may be identified in

20   accordance with the present inevntion. A variety of different assays are contemplated in this regard, including but not limited to, fluorescent *in situ* hybridization (FISH), direct DNA sequencing, PFGE analysis, Southern or Northern blotting, single-stranded conformation analysis (SSCA), RNAse protection assay, allele-specific oligonucleotide (ASO), dot blot analysis, denaturing gradient gel electrophoresis, RFLP and PCR™-

25   SSCP.

(i)   Primers and Probes

The term primer, as defined herein, is meant to encompass any nucleic acid that is capable of priming the synthesis of a nascent nucleic acid in a template-dependent

30   process. Typically, primers are oligonucleotides from ten to twenty base pairs in length, but longer sequences can be employed. Primers may be provided in double-stranded or

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single-stranded form, although the single-stranded form is preferred. Probes are defined differently, although they may act as primers. Probes, while perhaps capable of priming, are designed to binding to the target DNA or RNA and need not be used in an amplification process.

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In preferred embodiments, the probes or primers are labeled with radioactive species (^{32}P, ^{14}C, ^{35}S, ^{3}H, or other label), with a fluorophore (rhodamine, fluorescein) or a chemillumiscent (luciferase).

10   (ii)   Template Dependent Amplification Methods

A number of template dependent processes are available to amplify the marker sequences present in a given template sample. One of the best known amplification methods is the polymerase chain reaction (referred to as PCR™) which is described in detail in U.S. Patents 4,683,195, 4,683,202 and 4,800,159, and in Innis *et al.*, 1990, each

15 of which is incorporated herein by reference in its entirety.

Briefly, in PCR™, two primer sequences are prepared that are complementary to regions on opposite complementary strands of the marker sequence. An excess of deoxynucleoside triphosphates are added to a reaction mixture along with a DNA

20 polymerase, *e.g.*, *Taq* polymerase. If the marker sequence is present in a sample, the primers will bind to the marker and the polymerase will cause the primers to be extended along the marker sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the marker to form reaction products, excess primers will bind to the marker and to the reaction

25 products and the process is repeated.

A reverse transcriptase PCR™ amplification procedure may be performed in order to quantify the amount of mRNA amplified. Methods of reverse transcribing RNA into cDNA are well known and described in Sambrook *et al.*, 1989. Alternative methods for

30 reverse transcription utilize thermostable, RNA-dependent DNA polymerases. These

methods are described in WO 90/07641 filed December 21, 1990. Polymerase chain reaction methodologies are well known in the art.

Another method for amplification is the ligase chain reaction ("LCR"), disclosed in EPA No. 320 308, incorporated herein by reference in its entirety. In LCR, two complementary probe pairs are prepared, and in the presence of the target sequence, each pair will bind to opposite complementary strands of the target such that they abut. In the presence of a ligase, the two probe pairs will link to form a single unit. By temperature cycling, as in PCR™, bound ligated units dissociate from the target and then serve as "target sequences" for ligation of excess probe pairs. U.S. Patent 4,883,750 describes a method similar to LCR for binding probe pairs to a target sequence.

Methods based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide, may also be used in the amplification step of the present invention. Wu *et al.*, (1989), incorporated herein by reference in its entirety.

(iii)   Southern/Northern Blotting

Blotting techniques are well known to those of skill in the art. Southern blotting involves the use of DNA as a target, whereas Northern blotting involves the use of RNA as a target. Each provide different types of information, although cDNA blotting is analogous, in many aspects, to blotting or RNA species.

Briefly, a probe is used to target a DNA or RNA species that has been immobilized on a suitable matrix, often a filter of nitrocellulose. The different species should be spatially separated to facilitate analysis. This often is accomplished by gel electrophoresis of nucleic acid species followed by "blotting" on to the filter.

Subsequently, the blotted target is incubated with a probe (usually labeled) under conditions that promote denaturation and rehybridization. Because the probe is designed to base pair with the target, the probe will binding a portion of the target sequence under

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renaturing conditions. Unbound probe is then removed, and detection is accomplished as described above.

(iv)   Separation Methods

5   It normally is desirable, at one stage or another, to separate the amplification product from the template and the excess primer for the purpose of determining whether specific amplification has occurred. In one embodiment, amplification products are separated by agarose, agarose-acrylamide or polyacrylamide gel electrophoresis using standard methods. See Sambrook *et al.*, 1989.

10

Alternatively, chromatographic techniques may be employed to effect separation. There are many kinds of chromatography which may be used in the present invention: adsorption, partition, ion-exchange and molecular sieve, and many specialized techniques for using them including column, paper, thin-layer and gas chromatography (Freifelder,

15   1982).

(v)   Detection Methods

Products may be visualized in order to confirm amplification of the marker sequences. One typical visualization method involves staining of a gel with ethidium

20   bromide and visualization under UV light. Alternatively, if the amplification products are integrally labeled with radio- or fluorometrically-labeled nucleotides, the amplification products can then be exposed to x-ray film or visualized under the appropriate stimulating spectra, following separation.

25   In one embodiment, visualization is achieved indirectly. Following separation of amplification products, a labeled nucleic acid probe is brought into contact with the amplified marker sequence. The probe preferably is conjugated to a chromophore but may be radiolabeled. In another embodiment, the probe is conjugated to a binding partner, such as an antibody or biotin, and the other member of the binding pair carries a

30   detectable moiety.

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In one embodiment, detection is by a labeled probe. The techniques involved are well known to those of skill in the art and can be found in many standard books on molecular protocols. See Sambrook *et al.*, 1989. For example, chromophore or radiolabel probes or primers identify the target during or following amplification.

5

One example of the foregoing is described in U.S. Patent 5,279,721, incorporated by reference herein, which discloses an apparatus and method for the automated electrophoresis and transfer of nucleic acids. The apparatus permits electrophoresis and blotting without external manipulation of the gel and is ideally suited to carrying out

10   methods according to the present invention.

In addition, the amplification products described above may be subjected to sequence analysis to identify specific kinds of variations using standard sequence analysis techniques. Within certain methods, exhaustive analysis of genes is carried out

15   by sequence analysis using primer sets designed for optimal sequencing (Pignon *et al*, 1994). The present invention provides methods by which any or all of these types of analyses may be used. Using the sequences disclosed herein, oligonucleotide primers may be designed to permit the amplification of sequences throughout the MCIP genes that may then be analyzed by direct sequencing.

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(vi)   Kit Components

All the essential materials and reagents required for detecting and sequencing MCIP1, MCIP2 and MCIP3 and variants thereof may be assembled together in a kit. This generally will comprise preselected primers and probes. Also included may be

25   enzymes suitable for amplifying nucleic acids including various polymerases (RT, Taq, Sequenase[TM] *etc.*), deoxynucleotides and buffers to provide the necessary reaction mixture for amplification. Such kits also generally will comprise, in suitable means, distinct containers for each individual reagent and enzyme as well as for each primer or probe.

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B.   Immunologic Diagnosis

Antibodies of the present invention can be used in characterizing the MCIP content of healthy and diseased tissues, through techniques such as ELISAs and Western blotting. This may provide a screen for the presence or absence of cardiomyopathy or as

5   a predictor of heart disease.

The use of antibodies of the present invention, in an ELISA assay is contemplated. For example, anti-MCIP antibodies are immobilized onto a selected surface, preferably a surface exhibiting a protein affinity such as the wells of a

10   polystyrene microtiter plate. After washing to remove incompletely adsorbed material, it is desirable to bind or coat the assay plate wells with a non-specific protein that is known to be antigenically neutral with regard to the test antisera such as bovine serum albumin (BSA), casein or solutions of powdered milk. This allows for blocking of non-specific adsorption sites on the immobilizing surface and thus reduces the background caused by

15   non-specific binding of antigen onto the surface.

After binding of antibody to the well, coating with a non-reactive material to reduce background, and washing to remove unbound material, the immobilizing surface is contacted with the sample to be tested in a manner conducive to immune complex

20   (antigen/antibody) formation.

Following formation of specific immunocomplexes between the test sample and the bound antibody, and subsequent washing, the occurrence and even amount of immunocomplex formation may be determined by subjecting same to a second antibody

25   having specificity for MCIP1, MCIP2 or MCIP3 that differs the first antibody. Appropriate conditions preferably include diluting the sample with diluents such as BSA, bovine gamma globulin (BGG) and phosphate buffered saline (PBS)/Tween®. These added agents also tend to assist in the reduction of nonspecific background. The layered antisera is then allowed to incubate for from about 2 to about 4 hr, at temperatures

30   preferably on the order of about 25° to about 27°C. Following incubation, the antisera-contacted surface is washed so as to remove non-immunocomplexed material. A

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preferred washing procedure includes washing with a solution such as PBS/Tween®, or borate buffer.

To provide a detecting means, the second antibody will preferably have an associated enzyme that will generate a color development upon incubating with an appropriate chromogenic substrate. Thus, for example, one will desire to contact and incubate the second antibody-bound surface with a urease or peroxidase-conjugated anti-human IgG for a period of time and under conditions which favor the development of immunocomplex formation (e.g., incubation for 2 hr at room temperature in a PBS-containing solution such as PBS/Tween®).

After incubation with the second enzyme-tagged antibody, and subsequent to washing to remove unbound material, the amount of label is quantified by incubation with a chromogenic substrate such as urea and bromocresol purple or 2,2'-azino-di-(3-ethyl-benzthiazoline)-6-sulfonic acid (ABTS) and H_2O_2, in the case of peroxidase as the enzyme label. Quantitation is then achieved by measuring the degree of color generation, e.g., using a visible spectrum spectrophotometer.

The preceding format may be altered by first binding the sample to the assay plate. Then, primary antibody is incubated with the assay plate, followed by detecting of bound primary antibody using a labeled second antibody with specificity for the primary antibody.

The antibody compositions of the present invention will find great use in immunoblot or Western blot analysis. The antibodies may be used as high-affinity primary reagents for the identification of proteins immobilized onto a solid support matrix, such as nitrocellulose, nylon or combinations thereof. In conjunction with immunoprecipitation, followed by gel electrophoresis, these may be used as a single step reagent for use in detecting antigens against which secondary reagents used in the detection of the antigen cause an adverse background. Immunologically-based detection methods for use in conjunction with Western blotting include enzymatically-, radiolabel-,

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or fluorescently-tagged secondary antibodies against the toxin moiety are considered to be of particular use in this regard.

C.   Treating Defects in MCIP Expression or Function

5   The present invention also involves, in another embodiment, the treatment of disease states related to the aberrant expression and/or function of MCIPs. In particular, it is envisioned that reduced MCIP activity plays a role in cardiac failure through deregulation of calcineurin. Thus, increasing levels of MCIPs, or compensating for mutations that reduce or eliminate the activity of MCIPs, are believed to provide
10   therapeutic intervention in cardiomyopathies.

One of the therapeutic embodiments contemplated by the present inventors is the intervention, at the molecular level, in the events involved in cardiac failure. Specifically, the present inventors intend to provide, to a cardiac cell, an expression
15   construct capable of providing MCIP1, MCIP2 or MCIP3 to that cell. The lengthy discussion of expression vectors and the genetic elements employed therein is incorporated into this section by reference. Particularly preferred expression vectors are viral vectors such as adenovirus, adeno-associated virus, herpesvirus, vaccinia virus and retrovirus. Also preferred is liposomally-encapsulated expression vector.

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Those of skill in the art are well aware of how to apply gene delivery to *in vivo* situations. For viral vectors, one generally will prepare a viral vector stock. Depending on the kind of virus and the titer attainable, one will deliver 1×10^4, 1×10^5, 1×10^6, 1×10^7, 1×10^8, 1×10^9, 1×10^{10}, 1×10^{11} or 1×10^{12} infectious particles to the patient.
25   Similar figures may be extrapolated for liposomal or other non-viral formulations by comparing relative uptake efficiencies. Formulation as a pharmaceutically acceptable composition is discussed below. Various routes are contemplated, but local provision to the heart and systemic provision (intraarterial or intravenous) are preferred.

30   In another embodiment, it is contemplated that blocking of calcineurin's phosphatase activity also will prove beneficial in the treatment of heart disease. This

may be accomplished in one of several ways. First, by providing a phosphorylated version of a peptide containing the Ser108 site of MCIP1, one my simply overwhelm the ability of calcineurin to remove phosphates from endogenous MCIP1. Second, using a similar approach, an analog of this same peptide, with an unremovable phosphate group

5   may be used, effectively creating a "suicide substrate" for calcineurin. This approach also could be exploited using a mimetic (see above). Third, one could use the a peptide chimera containing MCIP1's Ser108 site as "bait," with the other portion of the chimera containing an molecule that binds to and/or cleaves calcineurin. And fourth, any of the preceding methods could be accomplished by using an expression construct encoding the

10 Ser108 peptide.

D.   Combined Therapy

In many clinical situations, it is advisable to use a combination of distinct therapies. Thus, it is envisioned that, in addition to the therapies described above, one

15 would also wish to provide to the patient more "standard" pharmaceutical cardiac therapies. Examples of standard therapies include so-called "beta blockers", anti-hypertensives, cardiotonics, anti-thrombotics, vasodilators, hormone antagonists, endothelin antagonists, calcium channel blockers, phosphodiesterase inhibitors, angiotensin type 2 antagonists and cytokine blockers/inhibitors. Also envisioned are

20 combinations with pharmaceuticals identified according to the screening methods described herein.

Combinations may be achieved by contacting cardiac cells with a single composition or pharmacological formulation that includes both agents, or by contacting the cell with two

25 distinct compositions or formulations, at the same time, wherein one composition includes the expression construct and the other includes the agent. Alternatively, gene therapy may precede or follow the other agent treatment by intervals ranging from minutes to weeks. In embodiments where the other agent and expression construct are applied separately to the cell, one would generally ensure that a significant period of time did not expire between the

30 time of each delivery, such that the agent and expression construct would still be able to exert an advantageously combined effect on the cell. In such instances, it is contemplated

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that one would contact the cell with both modalities within about 12-24 hours of each other and, more preferably, within about 6-12 hours of each other, with a delay time of only about 12 hours being most preferred. In some situations, it may be desirable to extend the time period for treatment significantly, however, where several days (2, 3, 4, 5, 6 or 7) to several

5   weeks (1, 2, 3, 4, 5, 6, 7 or 8) lapse between the respective administrations.

It also is conceivable that more than one administration of either a MCIP-1 or MCIP-2 gene, or the other agent will be desired. Various combinations may be employed, where MCIP is "A" and the other agent is "B", as exemplified below:

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A/B/A   B/A/B   B/B/A   A/A/B   B/A/A   A/B/B   B/B/B/A   B/B/A/B

A/A/B/B   A/B/A/B   A/B/B/A   B/B/A/A   B/A/B/A   B/A/A/B   B/B/B/A

15   A/A/A/B   B/A/A/A   A/B/A/A   A/A/B/A   A/B/B/B   B/A/B/B   B/B/A/B

Other combinations are contemplated as well.

E.   Formulations and Routes for Administration to Patients

20   Where clinical applications are contemplated, it will be necessary to prepare pharmaceutical compositions - expression vectors, virus stocks and drugs - in a form appropriate for the intended application. Generally, this will entail preparing compositions that are essentially free of pyrogens, as well as other impurities that could be harmful to humans or animals.

25

One will generally desire to employ appropriate salts and buffers to render delivery vectors stable and allow for uptake by target cells. Buffers also will be employed when recombinant cells are introduced into a patient. Aqueous compositions of the present invention comprise an effective amount of the vector to cells, dissolved or

30   dispersed in a pharmaceutically acceptable carrier or aqueous medium. Such compositions also are referred to as inocula. The phrase "pharmaceutically or

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pharmacologically acceptable" refer to molecular entities and compositions that do not produce adverse, allergic, or other untoward reactions when administered to an animal or a human. As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutically active substances is well know in the art. Except insofar as any conventional media or agent is incompatible with the vectors or cells of the present invention, its use in therapeutic compositions is contemplated. Supplementary active ingredients also can be incorporated into the compositions.

The active compositions of the present invention may include classic pharmaceutical preparations. Administration of these compositions according to the present invention will be via any common route so long as the target tissue is available via that route. This includes oral, nasal, buccal, rectal, vaginal or topical. Alternatively, administration may be by orthotopic, intradermal, subcutaneous, intramuscular, intraperitoneal or intravenous injection. Such compositions would normally be administered as pharmaceutically acceptable compositions, described *supra.*

The active compounds may also be administered parenterally or intraperitoneally. Solutions of the active compounds as free base or pharmacologically acceptable salts can be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion

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medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetable oils. The proper fluidity can be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial an antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

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For oral administration the polypeptides of the present invention may be incorporated with excipients and used in the form of non-ingestible mouthwashes and dentifrices. A mouthwash may be prepared incorporating the active ingredient in the required amount in an appropriate solvent, such as a sodium borate solution (Dobell's Solution). Alternatively, the active ingredient may be incorporated into an antiseptic wash containing sodium borate, glycerin and potassium bicarbonate. The active ingredient may also be dispersed in dentifrices, including: gels, pastes, powders and slurries. The active ingredient may be added in a therapeutically effective amount to a paste dentifrice that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants.

The compositions of the present invention may be formulated in a neutral or salt form. Pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like.

Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms such as injectable solutions, drug release capsules and the like. For parenteral administration in an aqueous solution, for example, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, sterile aqueous media which can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage could be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example,

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"Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580).
Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet sterility, pyrogenicity, general safety and purity standards as required by FDA Office of Biologics standards.

V.   Methods of Making Transgenic Mice

A particular embodiment of the present invention provides transgenic animals that contain MCIP-related constructs. Transgenic animals expressing MCIP1, MCIP2 and MCIP3, recombinant cell lines derived from such animals, and transgenic embryos may be useful in methods for screening for and identifying agents that modulate the function of MCIP1, MCIP2 or MCIP3, and thereby alleviate pathology related to the over or under expression of these molecules. The use of constitutively expressed MCIPs provides a model for over- or unregulated expression. Also, transgenic animals which are "knocked out" for MCIP1, MCIP2 and/or MCIP3.

A.   Methods of Producing Transgenics

In a general aspect, a transgenic animal is produced by the integration of a given transgene into the genome in a manner that permits the expression of the transgene. Methods for producing transgenic animals are generally described by Wagner and Hoppe (U.S. Patent 4,873,191; which is incorporated herein by reference), Brinster *et al.* 1985; which is incorporated herein by reference in its entirety) and in "Manipulating the Mouse Embryo; A Laboratory Manual" 2nd edition (eds., Hogan, Beddington, Costantimi and Long, Cold Spring Harbor Laboratory Press, 1994; which is incorporated herein by reference in its entirety).

Typically, a gene flanked by genomic sequences is transferred by microinjection into a fertilized egg. The microinjected eggs are implanted into a host female, and the progeny are screened for the expression of the transgene. Transgenic animals may be

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produced from the fertilized eggs from a number of animals including, but not limited to reptiles, amphibians, birds, mammals, and fish.

DNA clones for microinjection can be prepared by any means known in the art. For example, DNA clones for microinjection can be cleaved with enzymes appropriate for removing the bacterial plasmid sequences, and the DNA fragments electrophoresed on 1% agarose gels in TBE buffer, using standard techniques. The DNA bands are visualized by staining with ethidium bromide, and the band containing the expression sequences is excised. The excised band is then placed in dialysis bags containing 0.3 M sodium acetate, pH 7.0. DNA is electroeluted into the dialysis bags, extracted with a 1:1 phenol:chloroform solution and precipitated by two volumes of ethanol. The DNA is redissolved in 1 ml of low salt buffer (0.2 M NaCl, 20 mM Tris,pH 7.4, and 1 mM EDTA) and purified on an Elutip-D™ column. The column is first primed with 3 ml of high salt buffer (1 M NaCl, 20 mM Tris, pH 7.4, and 1 mM EDTA) followed by washing with 5 ml of low salt buffer. The DNA solutions are passed through the column three times to bind DNA to the column matrix. After one wash with 3 ml of low salt buffer, the DNA is eluted with 0.4 ml high salt buffer and precipitated by two volumes of ethanol. DNA concentrations are measured by absorption at 260 nm in a UV spectrophotometer. For microinjection, DNA concentrations are adjusted to 3 µg/ml in 5 mM Tris, pH 7.4 and 0.1 mM EDTA.

Other methods for purification of DNA for microinjection are described in Hogan *et al. Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1986), in Palmiter *et al. Nature* 300:611 (1982); in *The Qiagenologist, Application Protocols,* 3rd edition, published by Qiagen, Inc., Chatsworth, CA.; and in Sambrook *et al. Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989).

In an exemplary microinjection procedure, female mice six weeks of age are induced to superovulate with a 5 IU injection (0.1 cc, ip) of pregnant mare serum gonadotropin (PMSG; Sigma) followed 48 hours later by a 5 IU injection (0.1 cc, ip) of

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human chorionic gonadotropin (hCG; Sigma). Females are placed with males immediately after hCG injection. Twenty-one hours after hCG injection, the mated females are sacrificed by CO_2 asphyxiation or cervical dislocation and embryos are recovered from excised oviducts and placed in Dulbecco's phosphate buffered saline with

5   0.5% bovine serum albumin (BSA; Sigma). Surrounding cumulus cells are removed with hyaluronidase (1 mg/ml). Pronuclear embryos are then washed and placed in Earle's balanced salt solution containing 0.5 % BSA (EBSS) in a 37.5°C incubator with a humidified atmosphere at 5% CO_2, 95% air until the time of injection. Embryos can be implanted at the two-cell stage.

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Randomly cycling adult female mice are paired with vasectomized males. C57BL/6 or Swiss mice or other comparable strains can be used for this purpose. Recipient females are mated at the same time as donor females. At the time of embryo transfer, the recipient females are anesthetized with an intraperitoneal injection of

15   0.015 ml of 2.5 % avertin per gram of body weight. The oviducts are exposed by a single midline dorsal incision. An incision is then made through the body wall directly over the oviduct. The ovarian bursa is then torn with watchmakers forceps. Embryos to be transferred are placed in DPBS (Dulbecco's phosphate buffered saline) and in the tip of a transfer pipet (about 10 to 12 embryos). The pipet tip is inserted into the infundibulum

20   and the embryos transferred. After the transfer, the incision is closed by two sutures.

B.   Disease Models

Defects in MCIPs are believed to lead to increases in calcineurin activity. Therefore, it is contemplated that by reducing the expression and/or activity of MCIPs,

25   the activity of calcineurin will effectively be increased. Through earlier studies, overexpression of calcineurin has been shown to cause cardiac hypertrophy. Thus, in embodiments where it is desired that levels of calcineurin not be altered, it is still possible to create a hypertrophic situation by inhibiting or blocking MCIPs expression or activity.

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VI. Screening Assays

Thus, the present invention also contemplates the screening of compounds for various abilities to interact and/or affect MCIP1, MCIP2 and MCIP3 expression or function. Particularly preferred compounds will be those useful in inhibiting or promoting the binding of MCIP1, MCIP2 and MCIP3 to calcineurin. In the screening assays of the present invention, the candidate substance may first be screened for basic biochemical activity -- e.g., binding to a target molecule -- and then tested for its ability to inhibit modulate expression, at the cellular, tissue or whole animal level.

A.   Modulators and Assay Formats

i)   Assay Formats

The present invention provides methods of screening for modulators of MCIP1, MCIP2 and MCIP3 expression. In one embodiments, the present invention is directed to a method of:

(i)   providing a MCIP1, MCIP2 or MCIP3 polypeptide;

(ii)   contacting the MCIP1, MCIP2 or MCIP3 polypeptide with the candidate substance;

(iii)   contacting the MCIP1, MCIP2 or MCIP3 with calcineurin; and

(iv)   determining the binding of MCIP1, MCIP2 or MCIP3 polypeptide or calcineurin.

In another embodiment, this assay can be easily modified to look at the candidate substances effects on MCIP1, MCIP2 and/or MCIP3 binding to calcineurin. Another assay screens for MCIP1 dephosphorylation:

(a)   providing a phosphorylated MCIP1 and calcineurin;

(b)   admixing the MCIP1 and calcineurin in the presence of a candidate modulator;

(c)   assessing MCIP1 phosphorylation; and

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(d)   comparing the phosphorylation state of MCIP1 in step (c) with the phosphorylation state of MCIP1 in the absence of the candidate modulator.

A difference in MCIP phosphorylation in the presence of the candidate modulator, as compared to phosphorylation in the absence of said candidate modulator, identifies the candidate modulator as a modulator of MCIP phosphorylation.

In still another embodiment, the assay looks not at binding, but a MCIP expression. Such methods would comprise, for example:

(i)   providing a cell that expresses MCIP1, MCIP2 or MCIP3 polypeptide;

(ii)   contacting the cell with the candidate substance; and

(iii)   determining the effect of the candidate substance on expression of MCIP1, MCIP2 or MICP3 polypeptide.

It is not even necessary that MCIP be screened directly. Rather, a marker gene can be linked to an MCIP promoter. Expression of the marker protein, which is much easier to assay, is used as a surrogate for MCIP expression. In still other embodiments, one would look at the effect of a candidate substance on the mRNA synthesis, although alterations in mRNA stability and translation would not be accounted for.

In still yet another embodiment, one may look at one or more characteristics of a muscle cells to which a candidate substance is provided. This cell may be engineered in a variety of manners. First, it could be engineered for over- or underexpression of an MCIP, calcineurin or both. Second, it could be engineered to contain a marker gene under the control of a promoter that is regulated by calcineurin or some transcriptional activator downstream of calcineurin.

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ii)   Inhibitors and Activators

An inhibitor according to the present invention may be one which exerts an inhibitory effect on the expression of function of MCIP1, MCIP2 and/or MCIP3. By the same token, an activator according to the present invention may be one which exerts a stimulatory effect on the expression of function of MCIP1, MCIP2 and/or MCIP3.

iii)   Candidate Substances

As used herein, the term "candidate substance" refers to any molecule that may potentially modulate MCIP1, MCIP2 and/or MCIP3 expression or function. The candidate substance may be a protein or fragment thereof, a small molecule inhibitor, or even a nucleic acid molecule. It may prove to be the case that the most useful pharmacological compounds will be compounds that are structurally related to compounds which interact naturally with MCIP1, MCIP2 and/or MCIP3. Creating and examining the action of such molecules is known as "rational drug design," and include making predictions relating to the structure of target molecules.

The goal of rational drug design is to produce structural analogs of biologically active polypeptides or target compounds. By creating such analogs, it is possible to fashion drugs which are more active or stable than the natural molecules, which have different susceptibility to alteration or which may affect the function of various other molecules. In one approach, one would generate a three-dimensional structure for a molecule like a MCIP, and then design a molecule for its ability to interact with that MCIP. Alternatively, one could design a partially functional fragment of a MCIP (binding but no activity), thereby creating a competitive inhibitor. This could be accomplished by x-ray crystallography, computer modeling or by a combination of both approaches.

It also is possible to use antibodies to ascertain the structure of a target compound or inhibitor. In principle, this approach yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies to a functional, pharmacologically active antibody.

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As a mirror image of a mirror image, the binding site of anti-idiotype would be expected to be an analog of the original antigen. The anti-idiotype could then be used to identify and isolate peptides from banks of chemically- or biologically-produced peptides. Selected peptides would then serve as the pharmacore. Anti-idiotypes may be generated using the methods described herein for producing antibodies, using an antibody as the antigen.

In this case, there is ample evidence that demonstrates the binding of MCIPs to calcineurin. By analyzing the binding of MCIPs to this target molecule, much information can be gleaned about the ability of MCIPs to recognize calcineurin. With this information, predictions can be made regarding the structure of potential inhibitors or activators of MCIPs.

On the other hand, one may simply acquire, from various commercial sources, small molecule libraries that are believed to meet the basic criteria for useful drugs in an effort to "brute force" the identification of useful compounds. Screening of such libraries, including combinatorially generated libraries (e.g., peptide libraries), is a rapid and efficient way to screen large number of related (and unrelated) compounds for activity. Combinatorial approaches also lend themselves to rapid evolution of potential drugs by the creation of second, third and fourth generation compounds modeled of active, but otherwise undesirable compounds.

Candidate compounds may include fragments or parts of naturally-occurring compounds or may be found as active combinations of known compounds which are otherwise inactive. It is proposed that compounds isolated from natural sources, such as animals, bacteria, fungi, plant sources, including leaves and bark, and marine samples may be assayed as candidates for the presence of potentially useful pharmaceutical agents. It will be understood that the pharmaceutical agents to be screened could also be derived or synthesized from chemical compositions or man-made compounds. Thus, it is understood that the candidate substance identified by the present invention may be polypeptide, polynucleotide, small molecule inhibitors or any other compounds that may

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be designed through rational drug design starting from known inhibitors of hypertrophic response.

Other suitable inhibitors include antisense molecules, ribozymes, and antibodies (including single chain antibodies), each of which would be specific for a target located within the calcineurin pathway. Such compounds are described in greater detail elsewhere in this document.

It will, of course, be understood that all the screening methods of the present invention are useful in themselves notwithstanding the fact that effective candidates may not be found. The invention provides methods for screening for such candidates, not solely methods of finding them.

B.   In vitro Assays

A quick, inexpensive and easy assay to run is a binding assay. Binding of a molecule to a target may, in and of itself, be inhibitory, due to steric, allosteric or charge-charge interactions. This can be performed in solution or on a solid phase and can be utilized as a first round screen to rapidly eliminate certain compounds before moving into more sophisticated screening assays. In one embodiment of this kind, the screening of compounds that bind to a MCIP1, MCIP2 or MCIP3 molecule or fragment thereof is provided.

The target may be either free in solution, fixed to a support, expressed in or on the surface of a cell. Either the target or the compound may be labeled, thereby permitting determining of binding. In another embodiment, the assay may measure the inhibition of binding of a target to a natural or artificial substrate or binding partner (such as a MCIP). Competitive binding assays can be performed in which one of the agents (MCIP for example) is labeled. Usually, the target will be the labeled species, decreasing the chance that the labeling will interfere with the binding moiety's function. One may measure the amount of free label versus bound label to determine binding or inhibition of binding.

A technique for high throughput screening of compounds is described in WO 84/03564. Large numbers of small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with, for example, a MCIP and washed. Bound polypeptide is detected by various methods.

Purified target, such as a MCIP, can be coated directly onto plates for use in the aforementioned drug screening techniques. However, non-neutralizing antibodies to the polypeptide can be used to immobilize the polypeptide to a solid phase. Also, fusion proteins containing a reactive region (preferably a terminal region) may be used to link an active region (*e.g.*, the C-terminus of a MCIP) to a solid phase.

C.   *In cyto Assays*

Various cell lines that express MCIP1, MCIP2 and or MCIP3 can be utilized for screening of candidate substances. For example, cells containing a MCIP with an engineered indicators can be used to study various functional attributes of candidate compounds. In such assays, the compound would be formulated appropriately, given its biochemical nature, and contacted with a target cell.

Depending on the assay, culture may be required. As discussed above, the cell may then be examined by virtue of a number of different physiologic assays (growth, size, Ca^{++} effects). Alternatively, molecular analysis may be performed in which the function of a MCIP and related pathways may be explored. This involves assays such as those for protein expression, enzyme function, substrate utilization, mRNA expression (including differential display of whole cell or polyA RNA) and others.

D.   *In vivo Assays*

The present invention particularly contemplates the use of various animal models. Transgenic animals may be created with constructs that permit MCIP expression and activity to be controlled and monitored. The generation of these animals has been described elsewhere in this document.

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Treatment of these animals with test compounds will involve the administration of the compound, in an appropriate form, to the animal. Administration will be by any route the could be utilized for clinical or non-clinical purposes, including but not limited to oral, nasal, buccal, or even topical. Alternatively, administration may be by intratracheal instillation, bronchial instillation, intradermal, subcutaneous, intramuscular, intraperitoneal or intravenous injection. Specifically contemplated are systemic intravenous injection, regional administration via blood or lymph supply.

E.   *Production of Inhibitors*

In an extension of any of the previously described screening assays, the present invention also provide for method of producing inhibitors. The methods comprising any of the preceding screening steps followed by an additional step of "producing the candidate substance identified as a modulator of" the screened activity.

VII.   <u>EXAMPLES</u>

The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

Example 1

A.　Materials and Methods

5　　**Plasmid Constructs** -- An HA-tagged splice variant 4 of human MCIP1 (GenBank Accession No. U85267) was isolated from a human placental cDNA library by PCR using the primers:

5'-AGAACCATGCATTTTAGAAACTTTAACTACAGTTTTAG-3' and
10　5'-TAGAGCGTAGTCTGGGACGTCGTATGGGTAGCTGAGGTGGATCGGCG-3'

A c-myc-tagged splice variant 4 of mouse MCIP1 (GenBank Accession No. AA200984) was isolated from a mouse cardiac cDNA library by PCR using the primers:

15　5'-GAATTCCACCATGGAACAAAAACTTATTTCTGAAGAAGATCTGGATTTTA
　　　　GGGACTTTAGCTAC-3' and
　　　5'-GGATCCTCAGTTGGACACGGAGGGTGG-3'

A c-myc-tagged splice variant 1 of mouse MCIP1 (GenBank Accession No. AA734360)
20　was isolated from a mouse EST cDNA clone (Research Genetics, IMAGE 1223388) by PCR using the primers:

5'-GAATTCCACCATGGAACAAAAACTTATTTCTGAAGAAGATCTGGAGGAGG
　　　　TGGATCTGCAG-3' and
25　5'-GGATCCTCAGTTGGACACGGAGGGTGG-3'

A c-myc-tagged mouse MCIP2 (GenBank Accession No. AU035927) was isolated from the mouse EST clone MNCb-1054 (provided by K. Hashimoto, Japanese Collection of Research Bioresources, Tokyo, Japan) by PCR using the primers:

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5'-GAATTCCACCATGGAACAAAAACTTATTTCTGAAGAAGATCTGCCAGCC

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CCTAGCATGGAC-3' and

5'-GGATCCTCAGTTGGACACGGAGGGTGG-3'

The isolated PCR products described above were subcloned into mammalian expression plasmids pTARGETTM (Promega), or pEGFP-N1 (CLONTECH).

GST-MCIP1 fusions were expressed from the bacterial expression plasmid pGEX-CS (T.D. Parks, et al. 1994). Luciferase reporter plasmids, Mb-luc and IL-2-luc, were constructed in pGL3 (Promega) by inserting promoter/enhancer regions from genes encoding human myoglobin (Chin *et al.*, 1998) or IL-2 (Clipstone *et al.*, 1992), respectively. In addition, a synthetic enhancer consisting of three copies of a high affinity MEF2 binding sequence from the desmin promoter (Naya *et al.*, 2000) was linked to a minimal promoter (hsp68) and inserted into pGL3 yielding the des-MEF-luc reporter. The β-galactosidase reporter plasmid pCMV-lacZ (J. Grayson, et al. 1998), and expression vectors encoding constitutively active forms of NFAT (NFAT) (Molkentin *et al.*, 1998), calcineurin (CnA*) (Chin *et al.*, 1998, O'Keefe *et al.*, 1992), or calmodulindependent protein kinase type IV (CaMKIV) (Ho *et al.*, 1996), were previously described. The identity of plasmid constructions was confirmed by restriction mapping and partial DNA sequencing.

Tissue Culture, Cell Transfection, and Reporter Gene Assays -- C2C12 myoblasts were grown in Dulbecco's modified Eagle's medium supplemented with 20% fetal bovine serum and antibiotics (100 units of penicillin and 100 µg of streptomycin/ml). Myotube formation was induced by switching confluent cells to differentiation media (Dulbecco's modified Eagle's medium supplemented with 2% heat-inactivated horse serum) for 48-72 h. For transient transfection assays, C2C12 cells were plated 12 h before transfection in 12-well tissue culture dishes at 5×104 cells/well, and transfected with a total of 0.5 µg of plasmid DNA using LipofectAMINE Plus (Life Technologies, Inc.). Myoblasts were harvested 24 h after transfection. Myotubes were obtained by shifting cultures to differentiation media 24 h after transfection and harvesting 48 h later. To stimulate transfected cells, 1 µM ionomycin and 10 ng/ml

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phorbol myristate acetate (PMA) were added 4.5 h prior to harvesting. Luciferase assays of whole cell extracts were conducted as described previously (Yang *et al.,* 1997).

In Vitro **Protein-Protein Interaction Assays** -- GST and GST-MCIP1 fusion proteins were prepared as described previously (Grayson *et al.,* 1998). [^{35}S]Methionine labeled CnA398, CnA342, and CnA266 were produced in the TNT coupled *in vitro* transcription/translation system (Promega). For *in vitro* binding assays, equivalent amounts of GST fusion proteins bound to glutathione were resuspended in 500 µl of binding buffer (20 mM Tris, pH 7.5, 100 mM KCl, 0.1 mM EDTA, 0.05% Nonidet P-40, 10% glycerol, and 1 mg/ml bovine serum albumin). [^{35}S]Methionine-labeled CnA proteins were added to the resuspended GST fusion proteins and incubated for 1 h. The beads were then spun down and washed three times in binding buffer. An equal volume of 2× SDS-PAGE loading buffer was added, and the suspension was boiled for 3 min. The bound proteins were then resolved on SDS-PAGE and visualized by autoradiography. ^{35}S-Labeled luciferase protein (Promega) was used as a negative control. For estimation of binding efficiency, 25% of the radiolabeled protein was loaded as an input control.
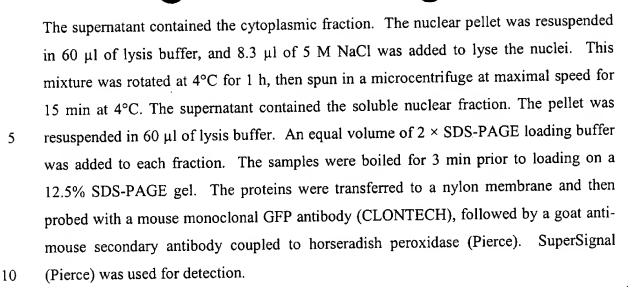
Fluorescence Microscopy -- An Olympus IMT-2 inverted fluorescence photomicroscope was used for evaluation and photography of C2C12 cells transfected with GFP expression plasmids. GFP fluorescence (excitation peak = 488 nm, emission peak = 507 nm) was photographed using an Optronics VI-470 CCD camera and a Power Macintosh G3 equipped with a Scion CG-7 frame grabber and Scion Image software.

Cell Fractionation -- C2C12 cells in 35-mm plates were transfected with mammalian expression plasmids encoding an activated form of calcineurin (CnA*) and MCIP1-GFP. Twenty-four hours after transfection, the cells were washed twice with ice-cold phosphate-buffered saline and then scraped from plates in 55 µl of ice-cold lysis buffer (20 mM HEPES, pH 7.4, 10 mM NaCl, 1.5 mM MgCl2, 20% glycerol, 0.1% Triton X-100, 1 mM dithiothreitol, and protease inhibitor mixture (Roche Molecular Biochemicals)). The cells were spun in a microcentrifuge at 1,000 rpm for 1 min at 4°C.

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The supernatant contained the cytoplasmic fraction. The nuclear pellet was resuspended in 60 μl of lysis buffer, and 8.3 μl of 5 M NaCl was added to lyse the nuclei. This mixture was rotated at 4°C for 1 h, then spun in a microcentrifuge at maximal speed for 15 min at 4°C. The supernatant contained the soluble nuclear fraction. The pellet was resuspended in 60 μl of lysis buffer. An equal volume of 2 × SDS-PAGE loading buffer was added to each fraction. The samples were boiled for 3 min prior to loading on a 12.5% SDS-PAGE gel. The proteins were transferred to a nylon membrane and then probed with a mouse monoclonal GFP antibody (CLONTECH), followed by a goat anti-mouse secondary antibody coupled to horseradish peroxidase (Pierce). SuperSignal (Pierce) was used for detection.

RNA Isolation and Analysis -- Total RNA was prepared from mouse tissues or C2C12 cells using RNAzol (Life Technologies, Inc.) following the manufacturer's protocol. Northern blot analysis was performed with 20 μg of total RNA in each lane and probed in Ultrahyb (Ambion) with a DNA fragment from the 3'-untranslated region of mouse MCIP1 isolated from a mouse EST clone (Research Genetics, IMAGE 1223388) by PCR using the primers (5'-GGCATCAGGTTATTCAGAGT-3' and 5'-GTGGAGTCCGTCGTAGCCAT-3') or the open reading frame of mouse MCIP2 cDNA.

B.   Results

Forced Expression of MCIP1 Blocks Calcineurin-Dependent Transcriptional Activation in Cultured Skeletal Myoblasts and Myotubes -- To determine whether MCIP alters calcineurin signaling in mammalian muscle cells, a mouse myoblast cell line, C2C12, was transfected with plasmid DNA constructs expressing human MCIP1 and a constitutively active form of calcineurin (CnA*) (O'Keefe *et al.*, 1992) along with luciferase reporter plasmids controlled either by a minimal promoter (TATA-luc) or two different calcineurin-responsive enhancer constructs from the human interleukin-2 (IL-2-luc) (Clipstone *et al.*, 1992) or myoglobin (Mb-luc) (Chin *et al.*, 1998) genes. The minimal TATA promoter was unresponsive to either CnA* or MCIP1 in both proliferating myoblasts and differentiated myotubes (FIG. 1A). Both the IL-2 and Mb
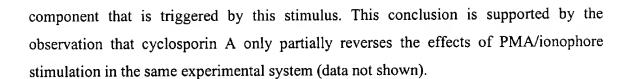
85

enhancer constructs were activated by CnA*, and this effect was abolished by forced expression of MCIP1. MCIP1 alone had no effect on the activity of any constructs.

It is interesting to note that calcineurin-dependent activation of the IL-2 enhancer is greater in proliferating myoblasts than in differentiating myotubes. Conversely, the muscle-specific Mb enhancer is more responsive in the differentiated cell background, probably reflecting a functional collaboration between NFAT and myogenic determination factors such as MEF2. MCIP reverses calcineurin-dependent activation of either enhancer at either developmental stage, suggesting that the mechanisms of inhibition are independent of the specific downstream effectors that are transducing the calcineurin signal.

The ability of MCIP to inhibit calcineurin-dependent gene transcription was distinguished from generalized transcriptional repression by analysis of a different reporter construct that is not influenced by calcineurin signaling. C2C12 cells were transfected with a luciferase reporter plasmid under the control of a multimerized Gal4p binding motif (UASg-TATA-luc). Forced expression of a fusion protein that links the DNA binding domain of Gal4p to the potent transactivation domain of VP16 (Gal4-VP16) increased reporter gene transcription markedly (FIG. 1B), but this induction was not affected by MCIP1.

MCIP1 Inhibits Endogenous Calcineurin Activated by PMA/Ionophore Stimulation -- The results in FIG. 1A-B indicate that overexpression of MCIP inhibits a constitutively active form of calcineurin, but a different design was required to determine whether this inhibitory function extends to the native protein. Endogenous calcineurin of C2C12 cells was stimulated as described previously in other cell types (Loh *et al.*, 1996) using a combination of phorbol myristate acetate (PMA) and a Ca2+ ionophore. PMA/ionophore stimulation activated the myoglobin enhancer (Mb-luc) in both myoblasts and myotubes (FIG. 2A), and this response was inhibited by co-transfection of the MCIP1 expression plasmid. The incomplete reversal by MCIP1 of Mb enhancer activity driven by PMA/ionophore may reflect a calcineurin-independent signaling

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component that is triggered by this stimulus. This conclusion is supported by the observation that cyclosporin A only partially reverses the effects of PMA/ionophore stimulation in the same experimental system (data not shown).

5   **MCIP1 Does Not Inhibit a Constitutively Active Form of NFAT** -- To distinguish an effect on calcineurin itself from an inhibitory mechanism acting upon downstream effectors of calcineurin signaling, the ability of MCIP1 to interfere with transcriptional activation driven by a variant form of NFAT that is constitutively active in the absence of calcineurin signaling (Rao *et al.*, 1997) was assessed. This variant of

10   NFATc, termed NFAT here, has been truncated to remove the amino-terminal regulatory domain, but retains DNA binding and transcriptional activation functions of the native protein. As a consequence of this truncation, NFAT is partitioned constitutively to the nuclear compartment, where it activates the IL-2 enhancer without a requirement for calcineurin activity (FIG. 2B). Forced expression of MCIP does not inhibit

15   transcriptional activation mediated by NFAT (FIG. 2B), in contrast to its effects on calcineurin-dependent transcription (FIGS. 1A-B and 2A-C). This result is interpreted to indicate that the inhibitory action of MCIP on calcineurin signaling is based on a direct interaction with calcineurin, rather than interference with downstream components of calcineurin-dependent signaling pathways.

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       MCIP Inhibits Calcineurin-dependent Regulation of MEF2 -- Previous experiments in (Chin *et al.*, 1998), and by others (Liu *et al.*, 1997, Mao *et al.*, 1999, Youn *et al.*, 1999), have indicated that the transactivating function of MEF2 transcription factors, in addition to NFAT proteins, is modified by calcineurin activity. The precise

25   mechanism of this response has not been elucidated, but this interaction can be demonstrated in a myocyte cell background using a MEF2-dependent reporter plasmid (des-MEF2-luc) constructed by linking three copies of a high affinity MEF2 binding site from the human desmin gene to a minimal promoter (Naya *et al.*, 2000). Transcription of the des-MEF2-luc reporter is up-regulated synergistically in skeletal myoblasts by

30   constitutively activated forms of calcineurin (CnA*) and calmodulin-dependent protein kinase IV (CaMKIV*) (FIG. 2C). In a manner similar to its effect on

calcineurindependent activation of the myoglobin and IL-2 promoter/reporter constructs (see FIGS. 1A-B), MCIP1 inhibited activation of the des-MEF2-luc reporter by CnA* alone, or by the combination of CnA* with CaMKIV (FIG. 2C). Since the des-MEF2-luc reporter lacks an NFAT binding site, the inhibitory effect of MCIP observed with this

5   reporter suggests that MCIP acts to inhibit the action of calcineurin on multiple substrates, rather than by interference that is limited to the NFAT:calcineurin interaction.

Multiple Members of the Family of MCIP Proteins Can Inhibit Calcineurin - - The human DSCR1 gene that encodes the protein now termed MCIP1 is composed of

10   seven exons (Fuentes et al., 1997). In humans, there are four splice variants each starting with a different initiating exon (1, 2, 3, or 4), followed by exons 5, 6, and 7. Splice variants 1 and 4 account for the vast majority of detectable transcripts. Exons 1 and 4 each encode the first 29 amino acids of proteins encoded by this gene and are more than 70% identical. Proteins produced from all splicing variations share the regions encoded

15   by exons 5-7. The splice variant of MCIP1 initiated by exon 4 (SEQ ID NOS: 20 and 21) was used in most of the experiments reported here. It has been determined, however, that proteins encoded by human splice variant 1 (SEQ ID NOS:18 and 19), and by murine splice variants 1 and 4 (SEQ ID NOS:12, 13, 14, 15), function similarly to inhibit calcineurin signaling to the myoglobin enhancer in a myocyte cell background (FIG. 3).

20   Likewise, the protein now termed MCIP2, encoded by the ZAKI-4 gene, is 70% identical to MCIP1 and inhibits calcineurin-dependent transcriptional activation in this co-transfection assay (FIG. 3).

MCIP1 Interacts with the Catalytic Domain of CnA -- Recombinant MCIP1

25   protein, or truncated forms thereof, were purified from bacterial cell lysates as fusion proteins linked to glutathione S-transferase (GST-MCIP1). Binding of GST-MCIP1 to calcineurin in a cell free environment was assessed using the constitutively active calcineurin variant (CnA398), or truncated forms thereof, that were expressed and metabolically labeled with [^{35}S]methionine in coupled *in vitro* transcription/translation

30   reactions.

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In vitro translated CnA(398) lacking the autoinhibitory domain (I) and part of the calmodulin binding site (M) forms a physical complex with GST-MCIP1 (FIGS. 4A-B). Deletion of the regions of CnA that bind calmodulin (M) and calcineurin B (B), as represented by CnA(342), did not disrupt the interaction with MCIP1. However, a protein that was truncated further to remove the carboxyl-terminal half of the catalytic domain of CAN (CnA(266)) was no longer capable of binding MCIP1. It is concluded, therefore, that MCIP interacts with the catalytic domain of calcineurin A. Binding of MCIP, therefore, may occlude the active site as a mechanism for the functional inhibition observed *in vivo*.

There are two regions of MCIP proteins that resemble motifs found in NFAT that mediate interactions with calcineurin (FIGS. 5A-B). The first of these is an SP repeat motif contained within a 30-amino acid region of MCIP that also is homologous to yeast REX1p (Kingsbury *et al.,* 1998). NFAT proteins include three sets of these repeats (Masuda *et al.,* 1995, Ho *et al.,* 1995, Hoey *et al.,* 1995), and it is dephosphorylation of serine residues within this region by calcineurin that results in nuclear localization and transcriptional activation by NFAT (Loh *et al.,* 1996, Shibasaki *et al.,* 1996, Luo *et al.,* 1996, Beals *et al.,* 1997 and Masuda *et al.,* 1997). MCIP1 has only one SP repeat motif, and it differs also from NFAT by including two versus three SP pairs (SPXXSPXXXXXXEE in MCIP versus SPXXSPXXSPXXXXX(E/D)(E/D) in NFAT). A second region of MCIP, PXIXXT, at amino acid residues 181-186 of MCIP1 resembles the NFAT PXIXIT motif that has been defined functionally as a calcineurin docking site (43, 44). Truncation of MCIP1 so as to delete the PXIXXT motif from the carboxyl terminus (GST-MCIP1-177) reduced binding of MCIP to CnA* but did not abolish it (FIGS. 5A-B). Further deletion of the carboxyl end of MCIP (GST-MCIP1-136), leaving the SP repeat intact, did not significantly reduce binding further. However, a truncation mutant that lacks both the PXIXXT motif and the SP repeat (GST-MCIP1-102) had lower affinity for binding calcineurin in this assay. The inventors conclude that both of these domains contribute to the calcineurin MCIP1 interaction.
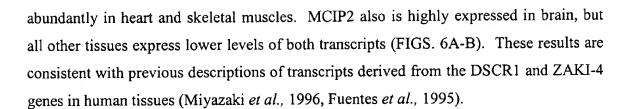
The Subcellular Localization of MCIP1 is Altered by Activated Calcineurin -
- A GFP-tagged human MCIP1 protein (MCIP-GFP) was expressed in C2C12 myoblasts to assess the subcellular distribution of MCIP1 in this cell background. Twenty hours after transfection, GFP-tagged MCIP1 was localized predominately to the nuclear compartment (FIG. 6A). After 48 h, very little of the MCIP-GFP protein remained. Co-transfection of plasmids encoding CnA* altered this pattern, such that after 24 h MCIP-GFP was observed predominately in the cytoplasm, and a fluorescent signal remained detectable for several days. The morphology of some cells suggested a nearly complete nuclear exclusion of MCIP-GFP in the presence of CnA* (FIG. 6B). Activation of endogenous calcineurin by addition of PMA/ionophore to the medium after transfection also resulted in the accumulation of MCIP-GFP in the cytoplasm (FIG. 6C). The subcellular distribution of native GFP was unaffected by co-expression of calcineurin.

C2C12 myoblasts transfected with MCIP-GFP were fractionated to separate cytoplasmic (C), soluble nuclear (S), and insoluble nuclear matrix (M) components. In the absence of activated calcineurin, MCIP1-GFP was present in both the nuclear soluble (S) and nuclear matrix (M) fractions. Expression of an activated form of calcineurin, CnA*, however, altered this association of MCIP1 with the nuclear matrix, such that soluble MCIP1 became detectable in both the soluble nuclear and cytoplasmic fractions (FIG. 6F). Overexpression of proteins in transfected cells can lead to a number of artifacts. Nevertheless, the effect of calcineurin expression on nuclear partitioning and chromatin binding of MCIP1 bolsters the conclusion that a physical interaction between MCIP1 and calcineurin is pertinent to the functional interactions that have been observed.

MCIP1 and MCIP2 are Expressed Most Abundantly in Striated Myocytes, and Their Expression is Up-regulated During Muscle Differentiation -- Gene-specific probes complementary to the 3'-untranslated regions of the mouse MCIP1 and MCIP2 cDNAs were used to examine expression of these genes in cultured myogenic cells and in tissues of adult mice. C2C12 myoblasts express low levels of MCIP1 mRNA transcript, but, upon differentiation of these cells into striated myotubes, expression increases severalfold (FIGS. 6A-B). In adult mice, MCIP1 and MCIP2 are expressed most

abundantly in heart and skeletal muscles. MCIP2 also is highly expressed in brain, but all other tissues express lower levels of both transcripts (FIGS. 6A-B). These results are consistent with previous descriptions of transcripts derived from the DSCR1 and ZAKI-4 genes in human tissues (Miyazaki *et al.*, 1996, Fuentes *et al.*, 1995).

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The analysis of MCIP1 and MCIP2 mRNAs in murine tissues also revealed differential expression of these transcripts among different skeletal muscle groups. The soleus muscle of the mouse (and other mammals) is enriched in slow, oxidative (Type I) myofibers, while the extensor digitorum longus is enriched in myofibers of the fast, glycolytic subtype (type IIb) (Schiaffino *et al.*, 1996). The expression of MCIP1 and MCIP2 is markedly increased in soleus muscle relative to extensor digitorum longus (FIGS. 6A-B), suggesting a selective activation of these genes in type I fibers. This result is particularly interesting in light of the evidence that calcineurin activity is an important determinant of the slow fiber phenotype (Chin *et al.*, 1998, Dunn *et al.*, 1999).

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Calcineurin-MCIP1 Double Transgenics Do Not Develop Cardiac Hypertrophy -- As previously reported, transgenic mice that contain calcineurin transgenes under the control of the α-MHC promoter develop massive cardiac hypertrophy. The inventors constructed α-MHC-MCIP1 transgenic mice. These mice appeared normal, although their hearts were slightly smaller than their wild-type littemates.

A cross was performed between the α-MHC-calcineurin transgenic mice and the alpha-MCH-MCIP1 transgenic mice. Mice carrying both transgenes appear normal. This striking result confirms the inventors' hypothesis that overexpression of MCIP1 is sufficient to prevent cardiac hypertrophy and heart failure. The data for two-month old male animals are as follows:

1661009.1

TABLE 4

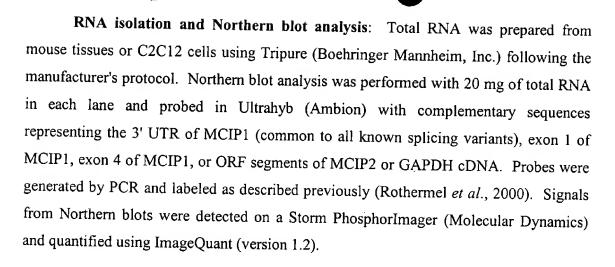| Genotype	Body Wt	Heart Wt	Heart Wt/Body Wt
α-MHC-Cal	25.5 g	.288 g	.0113
α-MHC-Cal/MCIP	24.0 g	.176 g	.0073

Example 2

A.   Materials and Methods

Plasmid constructions: The segment of intron 3 from the human MCIP1 (DSCR1) gene was isolated by PCR using human genomic DNA as template and primers based on sequence information from the human Chromosome 21 data bank (29).   This ~900 bp fragment was subcloned into a pGL3 luciferase reporter vector (Promega). Other plasmids were previously described (Chin *et al.*, 1998; Rothermel *et al.*, 2000).

Tissue culture, cell transfection or infection, reporter gene assays: C2C12 myoblasts and myotubes were cultured as previously described (Grayson *et al.*, 1995). Ionomycin (2 mM) and cyclosporin A (50 to 200 nM) were added 4 hrs prior to harvesting the cells. When included, cyclohexamide (25 mM) was added 15 min prior to ionomycin.   Transient transfection with plasmids or infection with recombinant, replication-defective adenoviruses, and luciferase assays were performed as previously reported (Chin *et al.*, 1998; Rothermel *et al.*, 2000; Wu *et al.*, 1973).

Animal experiments: Lines of transgenic mice in which the α myosin heavy chain promoter is used to drive expression of a constitutively active form of calcineurin selectively in the heart were generated and described previously (Molkentin *et al.*, 1998). Wildtype male C57Bl/6 mice were injected intraperitoneally with 3, 5, 3'-triiodothyromine (T3) (0.1 mg/g body weight) or an equal volume of 0.9% saline once a day for ten days (Robbins & Swain, 1992).   All experiments involving animals were conducted using IACRAC-approved protocols.

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RNA isolation and Northern blot analysis: Total RNA was prepared from mouse tissues or C2C12 cells using Tripure (Boehringer Mannheim, Inc.) following the manufacturer's protocol. Northern blot analysis was performed with 20 mg of total RNA in each lane and probed in Ultrahyb (Ambion) with complementary sequences representing the 3' UTR of MCIP1 (common to all known splicing variants), exon 1 of MCIP1, exon 4 of MCIP1, or ORF segments of MCIP2 or GAPDH cDNA. Probes were generated by PCR and labeled as described previously (Rothermel et al., 2000). Signals from Northern blots were detected on a Storm PhosphorImager (Molecular Dynamics) and quantified using ImageQuant (version 1.2).

cDNA microarray analysis of calcineurin-transgenic mice: RNA was isolated from two calcineurin-transgenic mice (Molkentin et al., 1998) at 10 weeks of age, and from a wild-type littermate. One of the transgenic mice was determined to be in heart failure, on the basis of anasarca with massive ascites, while the other appeared grossly normal. Both transgenic mice showed >100% increase in heart weight relative to the wildtype control (250 mg and 240 mg vs. 96 mg, respectively). Total body weights of the wildtype (26 g) and non-failing calcineurin transgenic mice (27.5 g) were comparable, while the calcineurin-transgenic mouse in heart failure had a greater body weight of 35.6 g, reflecting the edematous state. Microarray analyses were conducted by Incyte Genomics as described elsewhere (Schena et al., 1996). Briefly, polyA+ RNA was labeled with Cy3/Cy5 fluorescent dyes and hybridized with a mouse cDNA microarray (mouse GEM 1.14) containing 8,734 elements each (7,832 unique genes: 3336 annotated/ 4496 unannotated) genes. Differential expression was calculated as the ratio of fluorescent signals after subtraction of background.

B.   Results

Calcineurin induces expression of MCIP1 but not MCIP2: Gene expression profiling by microarray analysis was conducted to identify genes that are differentially regulated in hearts of transgenic mice engineered to express a constitutively active form of calcineurin, as compared to normal controls. Calcineurin-transgenic animals (α-MHC-CnA*) develop massive cardiac hypertrophy that progresses to dilated

cardiomyopathy3. This analysis identified MCIP1 as a gene that is potently up-regulated in this model (FIG. 7). Other genes known to be controlled by hypertrophic signals (*e.g.*, atrial natriuretic factor) also were identified by this analysis, and were induced to a comparable extent (approximately 3-fold) as MCIP1 in hypertrophic, non-failing hearts

5   of animals at 10 weeks of age, as compared to a wild-type littermate (FIG. 7, upper panel). Both MCIP1 and calcineurin A transcripts were elevated further in hearts of age-matched animals that had progressed to overt heart failure, compared to levels noted in hypertrophic, non-failing hearts (FIG. 7, lower panel). This induction of MCIP1 gene expression within the intact myocardium by activated calcineurin was confirmed by

10   Northern blot analysis. Quantitative estimates of the extent of MCIP1 induction in aMHC-CnA* hearts (Table 5) varied among individual animals of comparable age (3- to 17-fold), perhaps reflecting different stages in disease progression. Northern blots also revealed that the MCIP2 gene was not similarly regulated. In contrast to the up-regulation of MCIP1 mRNA in this model, there was no detectable change in MCIP2

15   mRNA (Table 5, right hand panel).

TABLE 5

Quantitative Estimates of Changes in MC1P1 and MC1P2 mRNA in Response to Calcineurin and Thyroid Hormone

A_1 Response to Calcineurin Activation				B_1 Response to Thyroid Hormone			
Stimulus	Tissue	MC1P1	MC1P2	Stimulus	Tissue	MC1P1	MC1P2
αMHC-CnA*	Heart	6.03	1.31	T3	Heart	1.05	1.59
	Heart	3.70	0.79	T3	Heart	0.87	1.81
	Heart	16.77	1.32	T3	Heart	1.08	1.71
CMV-CnA*	C2C12	1.48	ND	T3	Soleus	0.78	1.72
	C2C12	1.54	0.91	T3	Soleus	1.05	2.21
Ionomycin	C2C12	2.42	0.94	T3	Soleus	1.24	1.62
	C2C12	1.94	1.00				
	C2C12	1.26	1.12				
Can Effect		4.80±1.30	1.06±0.11	T3 Effect		1.01±0.06	1.78±0.01

Each line presents the fold change induced by the stimulus within a single experimental animal (heart), pooled muscles from two animals (soleus), or a single-cell culture dish (C2C12), quantified by PhosphorImager analysis of Northern blots in duplicate or triplicate, after background subtraction and normalization to a loading control (GAPDH mRNA). The aggregate effects of calcineurin (Can) and thyroid hormone (T3) are presented as mean values (±SE) of these 14 experiments.
ND indicates not determined.

The inventors also assessed the ability of calcineurin to stimulate expression of MCIP1 in C2C12 cells that differentiate into skeletal myotubes in cell culture. Increased intracellular calcium concentrations evoked by administration of the calcium ionophore ionomycin led rapidly (<4 hr) to an increased abundance of MCIP1 mRNA in C2C12 cells. MCIP1 mRNA is increased during differentiation of C2C12 cells (reported previously (Rothermel et al., 2000), not shown here), but a 2-fold induction of MCIP1 by ionomycin was evident irrespective of the stage of differentiation (myoblasts or myotubes) and the correspondingly lower or higher initial levels of MCIP1 mRNA. In contrast, expression of MCIP2 mRNA was unaffected by ionomycin (Table 5, left hand panel). To determine if the induction of MCIP1 gene expression by calcium ionophore was attributable to calcineurin activity, as opposed to other calcium-regulated signaling

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events, the inventors assessed the effects of cyclosporin A on this response. In a dose-dependent manner, cyclosporin A blocked the ability of ionomycin to up-regulate MCIP1 transcript levels in C2C12 cells, and even reduced MCIP1 transcripts below the levels observed in cells untreated with either drug, presumably by blocking basal as well as ionophore-stimulated calcineurin activity. Compared to cells treated with the highest dose of cyclosporin, MCIP1 mRNA was increased 4-fold by ionomycin in the absence of cyclosporin. In addition, MCIP1 mRNA was increased 2-fold in cultured myocytes by infection with a recombinant adenoviral vector encoding a constitutively activated form of calcineurin, as compared to the effects of infection by an control virus encoding Green Fluorescent Protein (GFP). Thus, experimental strategies based on loss-of-function and gain-of-function approaches in cultured myocytes support the conclusion that MCIP1 gene expression, but not that of MCIP2, is regulated by calcineurin signaling.

Induction of MCIP1 expression by calcineurin does not require new protein synthesis: In the presence of cyclohexamide, an inhibitor of protein synthesis, activation of calcineurin by ionomycin continued to up-regulate MCIP1 mRNA in C2C12 cells, indicating that this induction is not dependent on the generation of new proteins. The magnitude of ionomycin-stimulated up-regulation of MCIP1 in the presence of cyclohexamide (~10-fold) was greater than that observed when cyclohexamide was absent (~2-fold). The inventors interpret these data to support the hypothesis that calcineurin stimulates MCIP1 gene transcription by post-translational modification of a pre-existing pool of NF-AT proteins (and possibly other transcription factors). The greater magnitude of MCIP1 induction by calcineurin when new protein synthesis is blocked is potentially attributable to abrogation of calcineurin-dependent induction of endogenous MCIP1 synthesis, thereby eliminating negative feedback that otherwise would restrain calcineurin activity.

Thyroid hormone induces expression of MCIP2 but not MCIP1: The gene encoding MCIP2 was identified originally in a subtractive cloning experiment designed to identify genes that are up-regulated by thyroid hormone in cultured human fibroblasts (Miyazaki *et al.*, 1996). To determine whether MCIP genes are regulated by thyroid
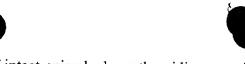
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hormone in hearts of intact animals, hyperthyroidism was induced in wildtype mice by intraperitoneal injection of T3 for ten days. As noted previously (Robbins & Swain, 1992), T3 treated hearts were uniformly hypertrophic (mean heart weight =180 mg versus 130 mg; mean heart weight/body weight ratio = 7.2 mg/gm versus 4.9 mg/gm; n=4 animals in each group). In contrast to the effects of activated calcineurin in the murine heart (FIG. 7), the expression of MCIP1 was unaltered in hyperthyroid hearts. However, MCIP2 transcript levels were increased approximately 2-fold in both heart and soleus skeletal muscles of T3-treated mice (Table 5, right hand panel). It remains to be determined whether the effects of T3 are a direct consequence of nuclear receptor binding to regulatory elements of the MCIP2 gene, or a result of indirect mechanisms.

An intragenic region located 5' to exon 4 of the MCIP1 gene is sufficient to promote a transcriptional response to calcineurin: The human MCIP1 gene (annotated initially as DSCR1) was reported to express four variant mRNAs with each of four alternative exons incorporated selectively at the 5' terminus of the expressed transcripts (Fuentes *et al.*, 1997). The majority of these transcripts were identified to represent isoforms that include sequences encoded either by exon 1 or exon 4 (Fuentes *et al.*, 1997). These variants have unique 5' UTR regions, and encode proteins that differ within the first 29 amino acids. The remaining 168 residues of MCIP1, encoded by exons 5-7, are identical in all MCIP1 variants (FIG. 8A). In experiments on hearts of transgenic mice, the inventors determined that expression of the exon 4 variant of MCIP1 mRNA was particularly sensitive to calcineurin activity. The increased abundance of MCIP1 mRNA detected by a probe complementary to the 3' UTR, which is included within all variants of MCIP1 (FIG. 8A), was mirrored by the increase detected with a probe complementary only to unique exon 4 sequences. In contrast, MCIP1 transcripts that include exon 1 sequences were present only at the limit of detection in wildtype murine hearts, and were not induced by the activated calcineurin transgene (not shown).

The selectively increased expression of the exon 4 variant of MCIP1 mRNA suggested the possibility of alternative promoter usage as a function of calcineurin activation, and the inventors sought to determine whether transcriptional regulatory

elements involved in transducing this signal reside in proximity to exon 4 of the MCIP1 gene. Accordingly, the inventors isolated a ~900 bp genomic segment from this position (-874 to +30 relative to the first nucleotide of exon 4). This region was found to contain a remarkably dense cluster of consensus NF-AT binding motifs (T/AGGAAANA/T/C)35

5 (FIG. 8A). A reporter plasmid was constructed to link this MCIP1 genomic region to a luciferase reporter gene (FIG. 8B), and this construct was tested for its ability to respond to calcineurin after transfection into C2C12 cells. Like the endogenous MCIP1 gene, expression of this transgene is increased by activated calcineurin (FIG. 8C), which has no effect on a control plasmid (minimal TATA plus luciferase; not shown). Inhibition of

10 calcineurin activity by concomitant over-expression of MCIP1 represses this response (not shown). Luciferase reporter plasmids controlled by shorter segments of this genomic region 5' to exon 4 (-231 to +30 or -163 to +30; FIG. 8B) retain basal activity equivalent to the -874 to +30 segment, but progressively lose calcineurin responsiveness as the number of NF-AT binding sites is reduced (FIG. 8C).

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Example 3

A. Materials and Methods

Plasmid constructs and generation of transgenic mice: A full length human

20 MCIP1 cDNA encoding the exon 4 splice variant of hMCIP1 with an HA epitope tag from the human influenza hemaglutinin protein (hMCIP1-HA) was cloned 3' to a 5.5 kb segment of the α-myosin heavy chain promoter (α-MHC) and 5' to a 0.6 kb polyadenylation signal from the human growth hormone gene (FIG. 10), carried in the pBluescriptII SK+ vector (Stratagene, La Jolla, CA). The transgene was linearized and

25 separated from prokaryotic sequences following digestion with NotI, and microinjected into fertilized oocytes from C57/BL6 mice, which were introduced into pseudopregnant females to generate lines of transgenic mice, using standard techniques. Animals were genotyped by Southern blot analysis of tail genomic DNA digested with EcoRI and probed with the hMCIP1 transgene. Animals carrying the α-MHC-hMCIP1 transgene

30 were crossed with transgenic mice expressing a constitutively activated form of calcineurin, also under the control of the α-MHC promoter (Gulick *et al.*, 1991) to

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produce doubly transgenic mice (α-MHC-hMCIP1 x α-MHC-CnA*). MCIP expression plasmids were constructed in the pTARGET vector (Promega, Madison, WI) under the control of the cytomegalovirus (CMV) promoter. pCMV-hMCIP1 encodes an HA-tagged full length hMCIP1 (amino acids 1-197). pCMV-ΔhMCIP1 encodes an HA-tagged
5   truncated hMCIP1 (amino acids 81 to 197). Other expression vectors and reporter genes have been previously described (Rothermel et al., 2000).

Cell culture studies: C2C12 myoblasts were maintained and transfected as previously described (Rothermel et al., 2000). Luciferase assays of whole cell extracts
10   were performed as previously described (Rothermel et al., 2000). All results were corrected for variations in transfection efficiency by normalization to expression of a cotransfected pCMV-LacZ plasmid.

Intact animal studies: In addition to the genetic cross to α-MHC-CnA* animals,
15   α-MHC-hMCIP1 transgenic mice and wild-type littermates were subjected to two independent stimuli known to provoke cardiac hypertrophy. Twelve-week old and 28-week old male mice were surgically implanted with a subcutaneous mini-osmotic pump (Alzet model 2001) that released isoproterenol in 0.9% NaCl at a rate of 28 mg per hour per 25 kg of body weight over a seven day period. Control pumps delivered a 0.9% NaCl
20   solution. Hearts were harvested on day eight. The heart body weight ratio (htw/bw) of isoproterenol-treated, animals were compared to the mean htw/bw ratio of age matched saline-treated animals of the same genotype. For exercise-induced hypertrophy, 28-week old male animals were placed in individual cages where they had free access to a running wheel. The number of revolutions was monitored continuously for 28 days. The animals
25   ran an average of 3 to 5 kilometers a day. The heart body weight ratios (htw/bw) of the exercised animals were compared to the mean htw/bw ratios of age-matched sedentary animals of the same genotype. A Wilcoxon rank sum test was used to determine statistically significant differences among treatment groups (p<0.05). All animal protocols were reviewed and approved by the appropriate institutional review boards.

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RNA isolation and analysis: Total RNA was prepared from mouse heart and skeletal muscle using RNAzol (Life Technologies, Rockville, MD) following the manufacturer's protocol. Northern blot analysis was performed with 20 mg of total RNA in each lane and probed in Ultrahyb (Ambion, Austin, TX) with a DNA fragment from the coding region of the human MCIP1 transgene. RNA dot blots prepared with 2 mg of total RNA were probed with end-labeled oligonucleotides specific for mouse GAPDH, α-MHC, β-myosin heavy chain (b-MHC), α-skeletal actin or atrial natriuretic factor (ANF). Bound probes were detected on a Storm PhosphorImager (Molecular Dynamics, Sunnyvalle, CA) and quantified using ImageQuant (version 1.2).

Western blot analysis: Protein extracts were made by homogenizing frozen mouse heart and skeletal muscle in phosphate buffered saline plus 20% glycerol, 1% Triton-X 100 and 1 mM DTT using a polytron homogenizer (Kinematica, Lucerne, Switzerland). Samples were boiled in protein loading buffer containing SDS, then passed over glass wool to remove DNA. Extracts were prepared from tissue culture cells by lysis directly in protein loading buffer. Proteins were separated by SDS-PAGE. Epitope-tagged, transgene-derived proteins were detected using a primary rat anti-HA monoclonal antibody (Roche, Nutley, NJ) and a horse radish peroxidase-tagged goat anti-rat secondary antibody (Bio-Rad, Hercules, CA).

Gross and histological analysis of hearts: Hearts were perfusion-fixed, embedded in paraffin and sectioned at 5 mm for histologic evaluation. Sections were stained with H&E and Masson's trichrome and photomicrographed using standard brightfield optics.

Transthoracic echocardiography: A 12 MHz probe (Hewlett Packard) was applied to the shaved chest wall of mice sedated with Avertin (0.1*0.15 cc/mg body weight) and maneuvered to obtain a parasternal short axis view of the left ventricular cavity. Two-dimensional and M-mode echocardiography images were digitized and stored on an optical disc. Data was collected using a sweep speed of 150. Fractional shortening (FS) was calculated from the Left Ventricular End Diastolic Dimension

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(LVEDD) minus the Left Ventricular End Systolic Dimension (LVESD) divided by the LVEDD.

B. Results

Expression and function of the α-MHC-hMCIP1 transgene product: Three independent lines of α-MHC-hMCIP1 transgenic mice were established. In all three of these lines, both mRNA and protein products of the transgene were expressed in hearts of animals in the F1 generation. However, the protein produced by the transgene was 14kD, much smaller than the predicted 24 kD full length hMCIP1 protein. Reverse transcriptase was used to generate a cDNA copy of the transgene product. The sequence of the cDNA demonstrated anomalous RNA splicing of the transgene from a cryptic splice donor site within the second non-coding exon of the α-MHC gene to an acceptor site within the hMCIP1 cDNA (illustrated in FIG. 10), thereby removing the authentic translational initiation codon. Fortuitously, a stable but truncated protein product is initiated from an internal, in-frame methionine codon at amino acid 81. This truncated MCIP1 protein accumulates to measurable levels within the heart.

To test whether the 14 kD transgene product inhibits calcineurin activity, the C2C12 myoblast cell line was transfected with a luciferase reporter gene driven by a calcineurin-responsive IL-2 promoter (IL-2-Luc). Cotransfection of a constitutively active calcineurin expression vector (pCMV-CnA*) with either an empty control vector (pCMV-neo) or a plasmid expressing a full length hMCIP1 (pCMV-hMCIP1) demonstrated the ability of hMCIP1 to almost completely inhibit calcineurin induction of the IL-2-Luc reporter gene (FIG. 11). A plasmid expressing the truncated cDNA from the transgene (pCMV-ΔhMCIP1) was as effective an inhibitor of calcineurin as the wild-type, full-length MCIP1 protein (FIG. 11), verifying that the truncated 14 kD transgene product found in the hearts of the α-MHC-hMCIP1 mice is a powerful inhibitor of calcineurin activity. Western analysis comparing cardiac ΔhMCIP1 protein levels in the three founder lines showed comparable transgenic protein levels in L1 and L3, whereas in the L2 line, ΔhMCIP1 protein levels were two to three times higher (data not shown).

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Strong cardiac-specific expression is initiated around the time of birth under the control of the α-MHC promoter (Gulick *et al.*, 1991). The α-MHC-hMCIP1 transgene was inherited in a normal 1-to-1 Mendelian ratio in L1 and L3 with no evidence of deleterious effects in adult mice. Transmission of the L2 transgene was slightly reduced

5 suggesting partial embryonic lethality, possibly due to embryonic expression of the transgene in this line. After birth however, L2 mice demonstrated normal growth and life spans. All subsequent experiments were done using animals from the L1 and L3 founder lines which performed comparably.

10 MCIP1 inhibits cardiac hypertrophy in a genetic model of cardiomyopathy. As reported previously (Molkentin *et al.*, 1998), the inventors observed massive cardiac hypertrophy in α-MHC-CnA* transgenic mice. The extent of hypertrophic growth induced by the α-MHC-CnA* transgenic was attenuated, however, by concomitant expression of the α-MHC-hMCIP1 transgene. Animals carrying the α-MHC-hMCIP1

15 transgene were viable and fertile, and exhibited no obvious cardiovascular abnormalities, with the exception of a mild (5-10%) reduction in cardiac mass compared to wild-type animals (Table 6). In mice bearing both the α-MHC-CnA* and α-MHC-hMCIP1 transgenes, the extent of cardiac hypertrophy was reduced to approximately 28% of the response noted with the α-MHC-CnA* transgene alone (Table 6). Using a Wilcoxon

20 rank sum test for two groups of independent samples of observations the α-MHC-CnA* x α-MHC-hMCIP1 double transgenic mice developed significantly less cardiac hypertrophy than the α-MHC-CnA* transgenic mice ($p < 0.01$). Expression of the hMCIP1 transgene also prevented dilated cardiomyopathy induced by the CnA* transgene, as assessed by transthoractic echocardiography of a matched set of four male

25 littermates (Table 7). Fractional shortening (FS) as an indication of the ejection volume of the heart was restored to wild-type levels in the α-MHC-hMCIP1 x α-MHC-CnA* double transgenic (FS = 0.63) compared to the animal carrying the α-MHC-CnA* transgene alone, in which cardiac contractility was greatly impaired (FS = 0.30). While the α-MHC-CnA* transgenic mice frequently suffer sudden death (Molkentin *et al.*,

30 1998), no such early mortality was apparent in the α-MHC-hMCIP1 x α-MHC-CnA*

double transgenic mice. In addition to reducing the morphological and functional consequences of the α-MHC-CnA* transgene, hMCIP1 over-expression reduced the re-induction of the fetal program of gene expression that is characteristic of this and other models of cardiac hypertrophy. The levels of β-MHC, α-skeletal actin and ANF transcripts were elevated in the α-MHC-CnA* transgenic hearts compared to wild-type hearts. In the α-MHC-hMCIP1 x α-MHC-CnA* double transgenic, both α-skeletal actin and ANF transcript levels were comparable to those found in wild-type hearts. Similarly, β-MHC expression, while greater than wild-type levels, was reduced relative to the levels detected in the hearts of α-MHC-CnA* mice.

TABLE 6

Heart Weight/Body Weight Ratios of Transgenic Mice

wild type	α-MHC-hMC1P1	α-MHC-CnA*	α-MHC-CnA* X α-MHC-hMC1P1
4.33±0.09 (n=16)	4.10±0.23 (n=26)	9.92±1.06 (n=5)	5.69±0.35 (n=7)

Data are calculated as heart weight/body weight (mg/g; mean ±SEM). The numbers of animals of each genotype that were tested are shown in parentheses. Wild type and α-MHC-hMC1P1 mice were 12-15 weeks of age. Median age of α-MHC-CnA* and α-MHC-hMC1P1 X α-MHC-CnA* mice was 12 weeks.

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TABLE 7

Echocardiographic Assessment of the Left Ventricular Chamger

Genotype	LVEDD[†] (cm)	LVESD (cm)	FS
wild type	0.237	0.081	0.66
α-MHC-hMC1P1	0.253	0.098	0.62
α-MHC-CnA*	0.479	0.339	0.30
α-MHC-CnA*Xα-MHC-hMC1P1	0.298	0.113	0.63

Data collected from 20 week old male littermates.

5   [†]LVEDD, left centricular end-diastolic dimension; LVESD, left ventricular end-systolic dimension: FS, fractional shortening; FS=(LVEDD-LVESD)/LVEDD

MCIP1 limits hypertrophic responses to other stimuli in intact animals. Calcineurin activation has been implicated in the progression of both pathological and

10   adaptive cardiac hypertrophy (Eto et al., 2000). Chronic administration, over a seven day period, of the β-adrenergic receptor agonist isoproterenol using implantable osmotic minipumps produced a modest degree of cardiac hypertrophy in male wild-type animals, as described previously (Friddle et al., 2000) (22.8 ± 1.95 percent increase in heart weight to body weight ratio). This hypertrophic response was diminished, though not

15   abolished, by transgenic over-expression of hMCIP1 (9.4 ± 0.87 % increase) (FIG. 12). Similarly, physiological adaptive hypertrophy resulting from 28 days of nocturnal wheel running in wild-type male mice was reduced in animals carrying the α-MHC-hMCIP1 transgene (29.2 ± 4.23 % increase in wild-type versus 12.3 ± 4.15 % increase in the transgenic animals) (FIG. 12). Using a Wilcoxon rank sum test for two groups of

20   independent samples of observations the α-MHC-hMCIP1 mice developed significantly less cardiac hypertrophy in response to either isoproterenol or exercise (p<0.05).

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All of the COMPOSITIONS and METHODS disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the COMPOSITIONS and METHODS and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

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The following references, to the extent that they provide exemplary procedural or other details supplementary to those set forth herein, are specifically incorporated herein by reference.

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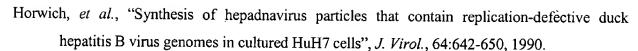Gomez-Foix *et al.*, *J. Biol. Chem.*, 267:25129-25134, 1992.

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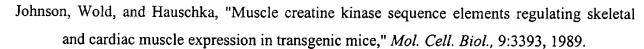
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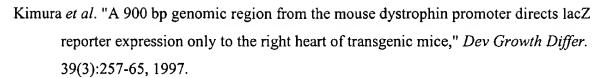
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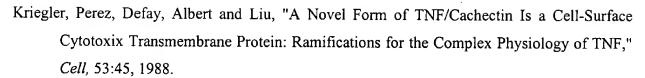
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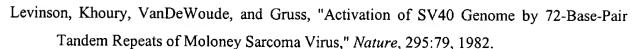
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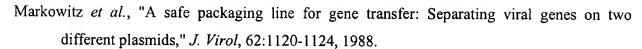
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